

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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STIC-Biotech/ChemLib

175918

LB

From: Kelly, Robert
Sent: Monday, January 09, 2006 8:22 AM
To: STIC-Biotech/ChemLib
Subject: 10/801,648

CITE

Please search:

- (i) nucleic acids matching SEQ ID NO: 1; and
- (ii) nucleic acids encoding SEQ ID NO: 2.

Robert M. Kelly, Ph.D.
Art Unit 1633
Room 2C55, Remsen Bldg.
Mailbox 2C70
(571) 272-0729

10801648

1-1547 NA
2-396a
LB

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 1-11
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Kelly, R.
10/801648

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 19:34:29 ; Search time 5436 Seconds
(without alignments)
16176.751 Million cell updates/sec

Title: US-10-801-648-1
Perfect score: 1547
Sequence: 1 ggggactcttgaacttgc.....aatacataatatatata 1547

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_ov.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_scs.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1547	100.0	1547	6	CQ875282 Sequence
2	1547	100.0	1547	6	CS031823 Sequence
3	1547	100.0	1547	6	CS040775 Sequence
4	1547	100.0	1547	6	I78455 Sequence 2
5	1547	100.0	1547	6	AX775087 Sequence
6	1547	100.0	1547	8	HUMBMP2A Human bone
7	1547	100.0	1581	6	CS038212 Sequence
8	1547	100.0	1607	6	AR157708 Sequence
9	1547	100.0	3526	6	AR447458 Sequence
10	1545.4	99.9	1607	6	AR031482 Sequence
11	1545.4	99.9	1607	6	AR130859 Sequence
12	1545.4	99.9	1607	6	AR353792 Sequence
13	1543.8	99.8	1607	6	I08630 Sequence 32
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15	1542.2	99.7	1547	6	CQ728408 Sequence
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18	1314.8	85.0	2154	6	AX201366 Sequence

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22	1227.2	79.3	1260	6	I83779	I83779 Sequence 4
23	1227.2	79.3	1260	6	AR308031	AR308031 Sequence
24	1227.2	79.3	1260	6	AR350343	AR350343 Sequence
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ALIGNMENTS

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DEFINITION	CQ875282	Sequence 25 from Patent WO2004076613.	1547 bp	DNA	linear	PAT 27-SEP-2004
ACCESSION	CQ875282	Sequence 25 from Patent WO2004076613.	1547 bp	DNA	linear	PAT 27-SEP-2004
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
	Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Herr, A., Hinzmann, B., Dahl, E., Staub, E., Pillarsky, C. and Specht, T.					
TITLE	Human nucleic acid sequences from carcinomas of the bladder					
JOURNAL	Patent: WO 2004076613-A 25 10-SEP-2004;					
	Herr, Alexander (DE); Hinzmann, Bernd (DE); Dahl, Edgar (DE);					
	Staub, Eike (DE); Pillarsky, Christian (DE); Specht, Thomas (DE)					
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RESULT 5
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LOCUS AX775087 1547 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 403 from Patent WO03038129.
ACCESSION AX775087
VERSION AX775087.1 GI:32486603
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE
AUTHORS Raponi, M.
TITILE Methods for assessing and treating leukemia
JOURNAL Patent: WO 03038129-A 403 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION M22489
ACCESSION M22489, 1 GI:179501
VERSION bone morphogenetic protein.
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SOURCE Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Wosney,J.M., Rosen,V., Celeste,A.J., Mitsock,L.M., Whitters,M.J.,
Kriz,R.W., Hewick,R.M. and Wang,E.A.
TITLE Novel regulators of bone formation: molecular clones and activities
JOURNAL Science 242 (4885), 1528-1534 (1988)
PUBMED 3201241
REFERENCE 2 (bases 1 to 1547)
AUTHORS Wosney,J.M., Rosen,V., Celeste,A.J., Mitsock,L.M., Whitters,M.J.,
Kriz,R.W., Hewick,R.M. and Wang,E.A.
JOURNAL Unpublished (1989)
COMMENT Original source text: Human osteosarcoma cell line U-2 OS, cDNA to
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[1] sites.
Draft entry and computer readable copy of sequence [1] kindly
submitted by R.W. Kriz 10-FEB-1989.

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QY	901	ACACACAGGTTGGTGAATCAGAATCAAGCAGGTGGGAAAGTTTTCATGTGCACCCCGCTG	960
Db	901	ACACACAGGTTGGTGAATCAGAATCAAGCAGGTGGGAAAGTTTTCATGTGCACCCCGCTG	960
QY	961	TGATCGGTGGACTGCAAGGACACGCCAACATGGATTCGTGGTGAAGTGGCCCACT	1020
Db	961	TGATCGGTGGACTGCAAGGACACGCCAACATGGATTCGTGGTGAAGTGGCCCACT	1020
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QY	1261	GGATTTGGTCTCCCGGGGTATCAGCCTTTTACTGCCACGGAGATGCCCTTTTCCTC	1320
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Db	1321	TGGCTGATCATCTGAATCCCACTAATCATGCCATTTGTCAGACGTTGGTCAACTCTGTATA	1380
QY	1381	ACTCTAAGATTCCTAAGGCATCTGTGTCGACGAACTCAGTGTCTATCTCGATGCTGT	1440
Db	1381	ACTCTAAGATTCCTAAGGCATCTGTGTCGACGAACTCAGTGTCTATCTCGATGCTGT	1440
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Db	1441	ACCTTGAACAGATGAAAGGTTGTTAAAGAACTATCAGACATGTTGTGGAGGTT	1500
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RESULT 7
CS038212
LOCUS CS038212 1581 bp DNA linear PAT 10-MAR-2005
DEFINITION Sequence 10 from Patent WO2005016368.
ACCESSION CS038212
VERSION CS038212.1 GI:60734760
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
Sfeir C., Campbell, P., Jadowiec, J.A. and Kumta, P.
METHOD OF INDUCING BIOMINERALIZATION, METHOD OF INDUCING BONE
REGENERATION AND METHODS RELATED THEREOF
Patent: WO 2005016368-A 10 24-FEB-2005;
University of Pittsburgh of the Commonwealth System of Hi gher
Education (US); Carnegie Mellon University (US)

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QY	421	TGCGGGCGGCTGCTGCGGGCGGCGGCTCTATCCAGCGCTCTGACGAGGCTCTGAGCG	480
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QY	541	CGTGGTCCCGCTTACATGCTAGACCTGTATCGAGGCACTCAGGTGAGCGGGCTCAC	600
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QY	601	CGGCCCCAGACCAACCGGTTGGAGAGGCGAGCCAGCGGAGCCCACTGTGCGCAGTTC	660
Db	601	CGGCCCCAGACCAACCGGTTGGAGAGGCGAGCCAGCGGAGCCCACTGTGCGCAGTTC	660
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QY	841	TTTATGAATCATATAAACCCTGCAACAGCCAACTCGAAATTCCTCCGTGACACAG	900
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QY	901	ACACACAGGTTGGTGAATCAGAATCAAGCAGGTGGGAAAGTTTTCATGTGCACCCCG	960
Db	901	ACACACAGGTTGGTGAATCAGAATCAAGCAGGTGGGAAAGTTTTCATGTGCACCCCG	960

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RESULT 8
AR157708
LOCUS AR157708 1607 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 3 from patent US 6245889.
ACCESSION AR157708
VERSION AR157708.1 GI:16218701
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1607)
AUTHORS Wang, E. A., Wozney, J. M. and Rosen, V. A.
TITLE BMP-4 products
JOURNAL Patent: US 6245889-A 3 12-JUN-2001;
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LOCUS AR447458 3526 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 11 from patent US 6673549.
ACCESSION AR447458
VERSION AR447458.1 GI:42675782
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3526)
AUTHORS Furness,L.M. and Buchbinder,J.L.
TITLE Genes expressed in C3A liver cell cultures treated with steroids
JOURNAL Patent: US 6673549-A 11 06-JAN-2004;
Incyte Corporation; Palo Alto, CA
FEATURES
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DEFINITION	Sequence 1 from patent US 5865364.		linear
ACCESSION	AR031482		PAT 29-SEP-1999
VERSION	AR031482.1	GI:5945771	

KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1607)
TITLE	Israel, D. and Wolfman, N.M.
JOURNAL	Recombinant bone morphogenetic protein heterodimers
FEATURES	Patent: US 5866364-A 1 02-FEB-1999;
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Qy	481	TCG	AGTTTGGCGCTGCTCAGCATGTTTCGGCTCTGAAACAGAGACCCCAACCCAGAGGGACG	540
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Qy	541	CCG	TGTTGCCCCCTCAATGCTAGACTGTATTCGACGGCACTCAGGTGACGCGGGCTCAC	600
Db	573	CCG	TGTTGCCCCCTCAATGCTAGACTGTATTCGACGGCACTCAGGTGACGCGGGCTCAC	632

QY	CGCCCCAGACCA	CCCGGTTGGAGAGGCGCAGCCAGCCGAGCCAA	CACGTGTGCGCAGCTTCC	660
DB	CGCCCCAGACCA	CCCGGTTGGAGAGGCGCAGCCAGCCGAGCCAA	CACGTGTGCGCAGCTTCC	692
QY	ACCATGAAGATCTTTTGGAGAAGACTACCAGAAA	CGAGTGGGAAAACAA	CCCGGAGATTCT	720
DB	ACCATGAAGATCTTTTGGAGAAGACTACCAGAAA	CGAGTGGGAAAACAA	CCCGGAGATTCT	752
QY	TCCTTTAATTAAAGTTCTATCCCA	CGGAGAGTTTATCACCTCAGCAGAGCTTTCAGGTTT	780	
DB	TCCTTTAATTAAAGTTCTATCCCA	CGGAGAGTTTATCACCTCAGCAGAGCTTTCAGGTTT	812	
QY	TCCGAGAACAGATGCAAGATGCTTTTAGAAAA	CAATAGCAGTTCCTCATCACCGAAATTAATA	840	
DB	TCCGAGAACAGATGCAAGATGCTTTAGAAAA	CAATAGCAGTTCCTCATCACCGAAATTAATA	872	
QY	TTTTATGAATCATATAAAACCTTGCAACG	CAACCTCGAAATTC	CCCGTGACCAAGACTTTTGG	900
DB	TTTTATGAATCATATAAAACCTTGCAACG	CAACCTCGAAATTC	CCCGTGACCAAGACTTTTGG	932
QY	ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTT	TGATGTCA	CCCCCGCTG	960
DB	ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTT	TGATGTCA	CCCCCGCTG	992
QY	TGATGCGGTGGACTGCA	CAGGGACAGCCCAACCATGGAATTCGTTGGTGAAGTGGCCCACT	1020	
DB	TGATGCGGTGGACTGCA	CAGGGACAGCCCAACCATGGAATTCGTTGGTGAAGTGGCCCACT	1052	
QY	TGGAGGAGAAACAAGGTGCTCC	NAGAGACATGTTAGGATAAGCAGGTCTTTG	CACCAAG	1080
DB	TGGAGGAGAAACAAGGTGCTCC	NAGAGACATGTTAGGATAAGCAGGTCTTTG	CACCAAG	1112
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DB	ATGAACACAGCTGGTCA	CAGATAAGGCCATTCGTAGTAACTTTTGGCCATGATGGAAG	1172	
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QY	ACTCTAGATTCCTTAAGGCATGCTGTG	TCCGACAGAACTCAGTGCTATCTCCATGCTGT	1440	
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QY	GTGGGTGTGCTAGTACAGCAAAATTA	ATAATAATATATATA	1547	
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RESULT 11
AR130859
LOCUS
DEFINITION
SEQUENCE 1 from patent US 6190890.
AR130859
ACCESSION
AR130859.1 GI:14119184
VERSION
KEYWORDS
linear
1607 bp
DNA
PAT 16-MAY-2001

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Qy	181	GAGAGGAGGAGGCAAGAAAGGAACGCAATTCGGTCTTTCGGCCACAGGTCTTTGACC	240		
Db	213	GAGAGGAGGAGGCAAGAAAGGAACGCAATTCGGTCTTTCGGCCACAGGTCTTTGACC	272		
Qy	241	AGAGTTTTCATGTGAGCGCTCTTTCAATGGACGTGTCCCGCGTGTCTTTAGACGGA	300		
Db	273	AGAGTTTTCATGTGAGCGCTCTTTCAATGGACGTGTCCCGCGTGTCTTTAGACGGA	332		
Qy	301	CTGCGGTCTCTAAAGGTTCGACCATGTGTGGCGCGGACCCGCTGTCTTAGCGTTGCTGC	360		
Db	333	CTGCGGTCTCTAAAGGTTCGACCATGTGTGGCGCGGACCCGCTGTCTTAGCGTTGCTGC	392		
Qy	361	TTCCCCAGGTCTCTCTGGCGCGCGGCTGGCTCTGTTTCGGAGCTGGCGCGCAGGAAGT	420		
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Qy	481	TCGAGTTTCGCGCTGTTCAGCATGTTCGGCTCTGAACAGAGACCCACCCAGCAGGACG	540		
Db	513	TCGAGTTTCGCGCTGTTCAGCATGTTCGGCTCTGAACAGAGACCCACCCAGCAGGACG	572		
Qy	541	CCGTGGTCCCGCTTACATGTAGACCTGTATCGCAGGCACTCAGGTCAGCGCGGCTCAC	600		
Db	573	CCGTGGTCCCGCTTACATGTAGACCTGTATCGCAGGCACTCAGGTCAGCGCGGCTCAC	632		
Qy	601	CGCCCCAGACCAACGGTTGAGAGGGCAGCCAGCCAGGACCAACTGTGCGCAGCTTCC	660		
Db	633	CGCCCCAGACCAACGGTTGAGAGGGCAGCCAGCCAGGACCAACTGTGCGCAGCTTCC	692		
Qy	661	ACCATGAAGATCTTTGGAAGAACTACAGAAACGAGTGGGAAACCAACCCCGAGATTCT	720		
Db	693	ACCATGAAGATCTTTGGAAGAACTACAGAAACGAGTGGGAAACCAACCCCGAGATTCT	752		
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Db	753	TCCTTAATTTAAGTTCTATCCCAACGAGGAGTTTATCACTCTCAGCAGAGCTTCAGGTTT	812		
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Db	813	TCCGAGAACAGATGCAAGATGCTTTAGGAACAATAGCAGTTTCCATCACCAGAAATTAATA	872		
Qy	841	TTTATGAATCATATAAACCTGCAACAGCCAACTCGAAATTCGCCGTGACAGACTTTGG	900		
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Db	933	ACACAGGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG	992		
Qy	961	TGATCGGTGACATGCAACAGGACACGCCAACCAATGGATTCGTGTGGAAGTGGCCCACT	1020		
Db	993	TGATCGGTGACATGCAACAGGACACGCCAACCAATGGATTCGTGTGGAAGTGGCCCACT	1052		
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Db	1053		TGAGGAGAAACAAGGTGTCTCCAGAGACATGTTAGGATTAAGCAGGTCTTTTGCA	CCAAAG	1112
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Db	1113		ATGAACACAGCTGTGTACAGATAAGGCCATTGCTAGTAACCTTTTGGCCATGATGGA	AAAAG	1172
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Db	1473		ACCTTGACGAGAAATGAAGTTGTATTAAAGAACTATCAGGACATGTTGTGAGGG	GTT	1532
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LOCUS					
DEFINITION Sequence 32 from Patent WO 880205.					
ACCESSION I08630					
VERSION I08630.1					
KEYWORDS GI:588673					
SOURCE Unknown.					
ORGANISM Unknown.					
REFERENCE Unclassified.					
AUTHORS 1 (bases 1 to 1607)					
TITLE Wang, B.A., Wozney, J.M. and Rosen, V.A.					
JOURNAL NOVEL OSTEOINDUCTIVE COMPOSITIONS					
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ORIGIN					
Query Match 99.8%; Score 1543.8; DB 6; Length 1607;					
Best Local Similarity 99.9%; Pred. No. 0;					
Matches 1545; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Qy	1	GGGACATCTTTGAATTTGACGGAGATAAATCTTGCGCACCCCACTTTTGCGCGGTGCTT	60		
Db	33	GGGACATCTTTGAATTTGACGGAGATAAATCTTGCGCACCCCACTTTTGCGCGGTGCTT	92		
Qy	61	TGCCCCAGCGAGCTGTTCGCCATCTCCAGACCCCAACCGCCCTCCACTCTCTCGGCT	120		
Db	93	TGCCCCAGCGAGCTGTTCGCCATCTCCAGACCCCAACCGCCCTCCACTCTCTCGGCT	152		
Qy	121	TGCCCCGACATGACAGCTGTTCAGCGTCAAGAGAGAGACTCGGCGCGCGCACCGG	180		
Db	153	TGCCCCGACATGACAGCTGTTCAGCGTCAAGAGAGAGACTCGGCGCGCGCACCGG	212		
Qy	181	GAGAGGAGGAGGCAAGAAAGGAACGCAATTCGGTCTTTCGGCCACAGGTCTTTGACC	240		

Db	213		GAGAAAGGAGGAGCAAAAGAAAGGAAACGGAATTCGGTCCCTTGCGCCAGGTCCTTTGACC	272
Qy	241		AGAGTTTTTCCATGTGGACGCTCTTTCAATGGAGAGTGTCCCGCGTGCTTTCTTAGACGGA	300
Db	273		AGAGTTTTTCCATGTGGACGCTCTTTCAATGGAGAGTGTCCCGCGTGCTTTCTTAGACGGA	332
Qy	301		CTGCGGCTCTCTAAAGGTGACCAATGFTGGCCGGGAACCGCTGTCTTCTTAGCGTTGCTGC	360
Db	333		CTGCGGCTCTCTAAAGGTGACCAATGFTGGCCGGGAACCGCTGTCTTCTTAGCGTTGCTGC	392
Qy	361		TTCCCCAGGTCCTCTGCGGCGCGCGGCTGCGCTCGTTCGGAGCTGGGCGGACGGAAGT	420
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Db	513		TCGAGTTGCGGCTGCTCAGCATGTTTGGCCCTGAAACACAGAGACCCACCCCCAGACGGAAG	572
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Db	573		CGTGGTGGCCCCCTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAGCCGGGCTCAC	632
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Qy	1381	ACTCTAAGATTCCTAAGGCATGCTGTGTCGCCGACAGAACTCAGTGCCTATCTCGATGCTGT	1440
Db	1413	ACTCTAAGATTCCTAAGGCATGCTGTGTCGCCGACAGAACTCAGTGCCTATCTCGATGCTGT	1472
Qy	1441	ACCTTGACGAGAAATGAAAGGTTCTGTTATTAAGAACTACTCAGGACATGTTGTGGAGGCTT	1500
Db	1473	ACCTTGACGAGAAATGAAAGGTTCTGTTATTAAGAACTACTCAGGACATGTTGTGGAGGCTT	1532
Qy	1501	GTGGGTGTGCTAGTACACGACAAAATTAATAATATATATATATATATA	1547
Db	1533	GTGGGTGTGCTAGTACACGACAAAATTAATAATATATATATATATA	1579
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LOCUS			
DEFINITION	BC069214	2041 bp mRNA linear	PRI 25-JUN-2004
ACCESSION	IMAGE:6303163	Homo sapiens bone morphogenetic protein 2, mRNA (cdna clone	
VERSION	BC069214	partial cds.	
KEYWORDS	BC069214.1	GI:46812656	
SOURCE			
ORGANISM		Homo sapiens (human)	
REFERENCE			
AUTHORS			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
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		Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, R.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, K.C., Jordan, H., Moore, T., Max, S.I., Wang, J., Heieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.D., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Woxley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, A.S., Krzywicki, M.I., Skalska, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.	
		Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
		Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
		12477932	
		2 (bases 1 to 2041)	
		Straussberg, R.	
		Direct Submission	
		Submitted (26-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
		NIH-MGC Project URL: http://mgc.nci.nih.gov	
		Contact: MGC help desk	
		Email: cgapps-remail.nih.gov	
		Tissue Procurement: Dr. Mark Watson	
		cDNA Library Preparation: Rubin Laboratory	
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)	
		DNA Sequencing by: Genome Sequence Centre,	
		BC Cancer Agency, Vancouver, BC, Canada	
		info@bcgsc.bc.ca	
		Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth	
REMARK			
COMMENT			

Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palquist, Anca Petrescu, Anna Liisa Pranhbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 54 Row: 1 Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1545; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGACTTCTTGAATTCGACGGAGATAACTTGGCACCCCACTTTTGGCGCGGTGCTT 60
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RESULT 15
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LOCUS
DEFINITION Sequence 14342 from Patent WO02068579.
ACCESSION Q0728408
VERSION Q0728408.1 GI:42297130
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE 1
 AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
 TITLE Kites, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof
 JOURNAL Patent: WO 02068579-A 14342 06-SEP-2002;
 PE Corporation (NY) (US)
 FEATURES Location/Qualifiers
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 Best Local Similarity 99.8%; Pred. No. 0;
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 Job time : 5444 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 16:30:58 ; Search time 679 Seconds
(without alignments)

15184.506 Million cell updates/sec

Title: US-10-801-648-1

Perfect score: 1547

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1547	100.0	1547	2	AaV01679 Bone morph
3	1547	100.0	1547	6	AbX90308 DNA encod
4	1547	100.0	1547	8	Abx76358 Lung canc
5	1547	100.0	1547	8	AcF34481 Gene enco
6	1547	100.0	1547	10	AcF05920 Human bon
7	1547	100.0	1547	10	AdD14609 Human src
8	1547	100.0	1547	10	AdE85186 Farnesyl
9	1547	100.0	1547	10	AdG63420 Human bon
10	1547	100.0	1547	10	AbT17041 Human MP2
11	1547	100.0	1547	10	AdL13510 Osteoar
12	1547	100.0	1547	11	AdN38841 Cancer/an
13	1547	100.0	1547	12	AdH11558 Human bon
14	1547	100.0	1547	12	AdK90635 Human CBM
15	1547	100.0	1547	12	AdO49064 Human ded
16	1547	100.0	1547	13	AdQ80231 Bone morph
17	1547	100.0	1547	13	AdR67125 Human bla
18	1547	100.0	1547	13	AdS73742 Human bon
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ALIGNMENTS

RESULT 1

AAQ32851

ID AAQ32851 standard; CDNA; 1547 BP.

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AC AAQ32851;

XX

DT 25-MAR-2003 (revised)

DT 05-MAY-1993 (first entry)

XX

DE BMP2.

XX

KW Bone; morphogenetic; protein; BMP; growth; vitamin D; systemic; treatment; dimer; ss.

XX

OS Rattus rattus.

XX

FN WO9221365-A1.

XX

PD 10-DEC-1992.

XX

PF 26-MAY-1992; 92WO-US004356.

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PR 05-JUN-1991; 91US-00709621.

XX

PR 27-MAR-1992; 92US-00856110.

XX

(PROC) PROCTER & GAMBLE CO.

XX

Stone RL;

XX

WPI; 1992-433371/52.

XX

Synergistic compan. for generating mammalian bone growth - comprises vitamin=D cpd. and bone morphogenetic protein.

XX

Disclosure; Page 27-29; 44pp; English.

XX

The sequences given in AAQ32850-56 encode bone morphogenetic proteins (BMP). BMP's increase bone growth and when used in conjunction with vitamin D the level of new bone growth is greater than when a BMP or vitamin D are used alone. The BMP's are administered for systemic treatment at a dose range of 1pg to 100 microg. BMP are active as dimers. (Updated on 25-MAR-2003 to correct PN field.)

CC

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XX SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Query Match 100.0%; Score 1547; DB 2; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 2
AAV01679
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XX AC AAV01679;
XX DT 25-MAR-2003 (revised)
XX DT 27-MAR-1998 (first entry)
XX DB Bone morphogenetic protein BMP-2 encoding DNA.
XX KW Bone morphogenetic protein; BMP; growth; vitamin D; fracture; arthritis;
XX KW surgical lesion; periodontal disease; osteoporosis; rickets; ds.
XX OS Unidentified.
XX PN US5693615-A.
XX PD 02-DEC-1997.
XX PF 23-JAN-1995; 95US-00377292.
XX PR 05-JUN-1991; 91US-00709621.
XX PR 27-MAR-1992; 92US-00856110.
XX PR 09-DEC-1992; 92US-00988363.
XX PR 07-SEP-1993; 93US-00117367.
XX PR 13-MAY-1994; 94US-00243435.
XX PA (PROC ) PROCTER & GAMBLE CO.
XX PI Stone RL;
XX DR WPI; 1998-031788/03.
XX XX
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PT Generation of new bone growth - by co-administering bone morphogenetic protein and vitamin D.

PS Claim 1; Col 19-22; 18pp; English.

A new method has been developed for generating new bone growth in a mammal. The method comprises administering a bone morphogenetic protein in combination with a vitamin D compound, where: (a) the bone morphogenetic protein is BMP-2 and is administered in an amount of 500-1000 ng in combination with about 6 ng vitamin D compound; or (b) the bone morphogenetic protein is BMP-4 and is administered in an amount of about 62.5 ng in combination with about 6 ng vitamin D compound. The present sequence encodes BMP-2. The method is used for treating bone defects or disorders, e.g. fractures, surgical lesions, periodontal disease, osteoporosis, arthritis and rickets. (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

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XX  
XX 18-JUL-2002.  
XX  
XX 11-JAN-2002; 2002WO-US000610.  
XX  
XX 12-JAN-2001; 2001US-0261252P.  
XX  
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
XX Langenfeld J;  
XX  
XX WPI; 2002-575416/61.  
XX  
XX Treating cancer, e.g. lung cancer, comprises administering a bone  
XX morphogenic protein-2 (BMP-2) activity inhibitor, or a vector encoding  
XX the inhibitor or an antisense oligonucleotide that binds to a BMP-2  
XX nucleic acid sequence.  
XX  
XX Disclosure; Page 37-40; 162pp; English.  
XX  
XX This invention relates to a novel method for treating cancer comprising  
XX administering to a patient a bone morphogenic protein-2 (BMP-2) activity  
XX inhibitor or an expression vector which has a nucleic acid sequence  
XX encoding the BMP-2 activity inhibitor or which encodes an antisense  
XX oligonucleotide that binds to a BMP-2 nucleic acid sequence. Inhibitors  
XX of BMP-2 activity encompassed in the invention are the proteins noggin,  
XX chordin, gremlin, cerberus 1 homologue and DAN. The method of the  
XX invention which utilises a BMP-2 activity inhibitor or an expression  
XX vector, is useful in diagnosing or treating cancers such as breast cancer  
XX or lung cancer. A kit is useful in the administration of the BMP-2  
XX activity inhibitor in the treatment of cancers. The present sequence  
XX represents the DNA encoding the human bone morphogenetic protein (BMP2)  
XX protein used in the method of the invention  
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1547; DB 6; Length 1547;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGACTTCTTGAATTCGAGGGAGAAATACTTGGCACCACCACTTTGGCCGGTGCCTT 60  
Db 1 GGGGACTTCTTGAATTCGAGGGAGAAATACTTGGCACCACCACTTTGGCCGGTGCCTT 60  
Qy 61 TGCCCCAGCGAGCTGCTCGCCATCTCCAGCGCCACCGCCCTCCACTCTCTCGGCCT 120  
Db 61 TGCCCCAGCGAGCGCTGCTCGCCATCTCCAGCGCCACCGCCCTCCACTCTCTCGGCCT 120  
Qy 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTCAAAAGAGAGACTCGCGCGCGGACCCGG 180  
Db 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTCAAAAGAGAGACTCGCGCGCGGACCCGG 180  
Qy 181 GAGAAGGAGGAGGCAAGAAAAGAAACGACATTCGGTCTTTGGCCGACGGTCTTTGACC 240  
Db 181 GAGAAGGAGGAGGCAAGAAAAGAAACGACATTCGGTCTTTGGCCGACGGTCTTTGACC 240
```

```
Qy 241 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGAGCGTGTCCCGCGTCTTCTTTAGACGGA 300  
Db 241 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGAGCGTGTCCCGCGTCTTCTTTAGACGGA 300  
Qy 301 CTGCGGTCTCTAAAGTTCGACCATGTGTGGCCGGGACCCGCTGTCTTTCTATAGCGTTGCTGC 360  
Db 301 CTGCGGTCTCTAAAGTTCGACCATGTGTGGCCGGGACCCGCTGTCTTTCTATAGCGTTGCTGC 360  
Qy 361 TTCCCAAGGTCTCTCTGGGCGGCGCGCTGGCTCTGTTCGAGAGCTGGGCGGACGGAAGT 420  
Db 361 TTCCCAAGGTCTCTCTGGGCGGCGCGCTGGCTCTGTTCGAGAGCTGGGCGGACGGAAGT 420  
Qy 421 TCGCGGCGGCGTGTCTGGGCGGCGCGCTCATCCAGAGCCTCTGAGAGGTCCTGAGCCAGT 480  
Db 421 TCGCGGCGGCGTGTCTGGGCGGCGCGCTCATCCAGAGCCTCTGAGAGGTCCTGAGCCAGT 480  
Qy 481 TCGAGTTGCGGCTGTCTCAGCATGTTCGGCTCTGAAAACAGAGACCCACCCGACGAGGACG 540  
Db 481 TCGAGTTGCGGCTGTCTCAGCATGTTCGGCTCTGAAAACAGAGACCCACCCGACGAGGACG 540  
Qy 541 CGGTGTGCCCCCTACATGCTAGACCTGTATGCGAGGCACTCAGGTCAGCCGGGCTCAC 600  
Db 541 CGGTGTGCCCCCTACATGCTAGACCTGTATGCGAGGCACTCAGGTCAGCCGGGCTCAC 600  
Qy 601 CCGCCCGAGACCAACCGGTTGGAGAGGCGCAGCCGAGCCCAACACTGTGCGAGCTTCC 660  
Db 601 CCGCCCGAGACCAACCGGTTGGAGAGGCGCAGCCGAGCCCAACACTGTGCGAGCTTCC 660  
Qy 661 ACCATGAAGAATCTTTGGAAAGAACTACAGAAACGAGTGGGAAAACAAACCGGAGATTCT 720  
Db 661 ACCATGAAGAATCTTTGGAAAGAACTACAGAAACGAGTGGGAAAACAAACCGGAGATTCT 720  
Qy 721 TCTTTAATTAAGTTCTATCCCGAGGAGTTTATCCTCAGAGAGCTTCAGGTTT 780  
Db 721 TCTTTAATTAAGTTCTATCCCGAGGAGTTTATCCTCAGAGAGCTTCAGGTTT 780  
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCCCGAATTATA 840  
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCCCGAATTATA 840  
Qy 841 TTTATGAAATCATAAAAACCTGCAACAGCCAACTCGAAATTCGCCGTGACCAAGATTGG 900  
Db 841 TTTATGAAATCATAAAAACCTGCAACAGCCAACTCGAAATTCGCCGTGACCAAGATTGG 900  
Qy 901 ACACGAGTTGGTGAATCAGAAATGCAAGAGTGGGAAAAGTTTGTATGTCAACCCCGCTG 960  
Db 901 ACACGAGTTGGTGAATCAGAAATGCAAGAGTGGGAAAAGTTTGTATGTCAACCCCGCTG 960  
Qy 961 TGATGCGGTGAGCTGTCACAGGACACGCCCAACCATGATTCGTGTTGAGTGGCCCACT 1020  
Db 961 TGATGCGGTGAGCTGTCACAGGACACGCCCAACCATGATTCGTGTTGAGTGGCCCACT 1020  
Qy 1021 TGGAGGAGAAAACAAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAG 1080  
Db 1021 TGGAGGAGAAAACAAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAG 1080  
Qy 1081 ATGAAACACAGCTGGTCAAGATAGGCCATTTGTAGTAACTTTTGGCCATGATGGAAG 1140  
Db 1081 ATGAAACACAGCTGGTCAAGATAGGCCATTTGTAGTAACTTTTGGCCATGATGGAAG 1140  
Qy 1141 GGCATCTCTCCACAAAGAGAAAACGTCAGCCAAACCAACACACGCGGAAACGCTTAA 1200  
Db 1141 GGCATCTCTCCACAAAGAGAAAACGTCAGCCAAACCAACACACGCGGAAACGCTTAA 1200  
Qy 1201 AGTCCAGCTGTGAAGACACCCCTTTGTACGTGGACTTCAGTACGTTGGGTGGAATGACT 1260  
Db 1201 AGTCCAGCTGTGAAGACACCCCTTTGTACGTGGACTTCAGTACGTTGGGTGGAATGACT 1260  
Qy 1261 GGATGTGGCTCCCCCGGGGTATCACGCCCTTTTACTGCCAGGAGATGCCCTTTTCTC 1320  
Db 1261 GGATGTGGCTCCCCCGGGGTATCACGCCCTTTTACTGCCAGGAGATGCCCTTTTCTC 1320
```

QY 1321 TGGCTGATCATCTGAACCTCCACTAATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCCACTAATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTA 1380
QY 1381 ACTCTAAGATTCCTTAAGGATGCTGTGTGCCGACAGAACTCAAGTCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTCCTTAAGGATGCTGTGTGCCGACAGAACTCAAGTCTATCTCGATGCTGT 1440
QY 1441 ACCTTGACGAGAAATGAAAGGTTGTTAATTAAGAACTATCAGGACATGTTGTGGAGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAAGGTTGTTAATTAAGAACTATCAGGACATGTTGTGGAGGTT 1500
QY 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAATACATAAATATATATATA 1547
Db 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAATACATAAATATATATATA 1547

RESULT 4

ABX76358
ID ABX76358 standard; DNA; 1547 BP.
XX
XX
AC ABX76358;
XX
XX
DT
XX
DE
XX
XX
Lung cancer-associated polynucleotide #222.
XX
Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350668P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Aziz N, Murray R;
PI
XX
XX WPI; 2003-093161/08.
DR P-PSDB; ABUS6629.
XX
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
XX
PS Claim 22; Page 357; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridizes
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell

CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC invention
XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Query Match 100.0%; Score 1547; DB 8; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGACTTCTTGAACCTTCAGGAGAAATACTTGGGCAACCCACATTTGGCGCGGTCCTT 60
Db 1 GGGGACTTCTTGAACCTTCAGGAGAAATACTTGGGCAACCCACATTTGGCGCGGTCCTT 60
QY 61 TGCCCGACGCGAGCTGCTTCGCCATCTCCGAGCCCCACCGCCCTCCACTCTCTCGGCT 120
Db 61 TGCCCGACGCGAGCTGCTTCGCCATCTCCGAGCCCCACCGCCCTCCACTCTCTCGGCT 120
QY 121 TGCCCGACACCTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCCGCGCACCCGG 180
Db 121 TGCCCGACACCTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCCGCGCACCCGG 180
QY 181 GAGAAGAGGAGGCAAGAAAGGAAACGGAATTCGCTTCCTTGGCCCAAGTCTCTTTGACC 240
Db 181 GAGAAGAGGAGGCAAGAAAGGAAACGGAATTCGCTTCCTTGGCCCAAGTCTCTTTGACC 240
QY 241 AGAGTTTTTCCATGTGGACGCTCTTCAATGAGAGCTGTCGCCGCTGCTTCTAGACGGA 300
Db 241 AGAGTTTTTCCATGTGGACGCTCTTCAATGAGAGCTGTCGCCGCTGCTTCTAGACGGA 300
QY 301 CTGCGGCTCTCTAAAGGTGACCATGTGTGGCGGGGACCCCGCTGTCTTCTAGCGTTGCTGC 360
Db 301 CTGCGGCTCTCTAAAGGTGACCATGTGTGGCGGGGACCCCGCTGTCTTCTAGCGTTGCTGC 360
QY 361 TTCCCGCAGGTCTCTCTGGCGCGCGGCTGCGCTGCTTTCGAGAGTGGCGCGCAGGAGT 420
Db 361 TTCCCGCAGGTCTCTCTGGCGCGCGGCTGCGCTGCTTTCGAGAGTGGCGCGCAGGAGT 420
QY 421 TCGCGGGGCGCTGCTGCGGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT 480
Db 421 TCGCGGGGCGCTGCTGCGGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT 480
QY 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTTGAAACAGAGACCCACCCCGCAGCGGAG 540
Db 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTTGAAACAGAGACCCACCCCGCAGCGGAG 540
QY 541 CCGTGGTGCCTCCCTATCATGTAGACCTGTATGCGAGGCACTCAGGTGAGCGCGGCTCAC 600
Db 541 CCGTGGTGCCTCCCTATCATGTAGACCTGTATGCGAGGCACTCAGGTGAGCGCGGCTCAC 600
QY 601 CGGCCCCAGACACCGGTTGGAGGGGCGAGCCGCGGAGCCCAACTGTGCGCAGCTCC 660
Db 601 CGGCCCCAGACACCGGTTGGAGGGGCGAGCCGCGGAGCCCAACTGTGCGCAGCTCC 660
QY 661 ACCATGAAGAAATCTTTGGAAGAACTTACCAGAAACGAGTGGGAAAAACAACCCGAGATTCT 720
Db 661 ACCATGAAGAAATCTTTGGAAGAACTTACCAGAAACGAGTGGGAAAAACAACCCGAGATTCT 720
QY 721 TCTTTAAATTTAAGTTCTATCCCGAGGAGGTTTATCACTCTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAAATTTAAGTTCTATCCCGAGGAGGTTTATCACTCTCAGCAGAGCTTCAGGTTT 780
QY 781 TCCGAGACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAAATAATA 840
Db 781 TCCGAGACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAAATAATA 840
QY 841 TTTTGAATCATATAAATCTGCAACAGGCAACTCGAAATTCGCCGTCACGAGACTTTTGG 900
Db 841 TTTTGAATCATATAAATCTGCAACAGGCAACTCGAAATTCGCCGTCACGAGACTTTTGG 900

QY 421 TCGCGCGCGTGTGTCGCGCGCGCCCTCATCCAGCCCTCTGACGAGGTCTCTGACGCGAGT 480
Db 421 TCGCGCGCGTGTGTCGCGCGCGCCCTCATCCAGCCCTCTGACGAGGTCTCTGACGCGAGT 480
QY 481 TCGAGTTCGGGTGTCTACGATGTTTCGGCTGTGAACACAGAGACCCACCCCGACGAGGACG 540
Db 481 TCGAGTTCGGGTGTCTACGATGTTTCGGCTGTGAACACAGAGACCCACCCCGACGAGGACG 540
QY 541 CGGTGTCGCCCTTACATGCTTAGACCTGTATCGCAGGCACTTCAGGTTCAGCGGGCTCAC 600
Db 541 CGGTGTCGCCCTTACATGCTTAGACCTGTATCGCAGGCACTTCAGGTTCAGCGGGCTCAC 600
QY 601 CGCGCCACAGACACCGTTCGGAGAGGCGAGCCGAGCCAGCAACACTGTGCGCAGCTTCC 660
Db 601 CGCGCCACAGACACCGTTCGGAGAGGCGAGCCGAGCCAGCAACACTGTGCGCAGCTTCC 660
QY 661 ACCATGAAGAATCTTTTGAAGAACTACACAGAAACGAGTGGGAAACAAACCCGAGATTCT 720
Db 661 ACCATGAAGAATCTTTTGAAGAACTACACAGAAACGAGTGGGAAACAAACCCGAGATTCT 720
QY 721 TCTTTAAATTAAGTTCTATCCCGAGGAGGTTTATCAGCTTCAGGAGCTTCAGGTTT 780
Db 721 TCTTTAAATTAAGTTCTATCCCGAGGAGGTTTATCAGCTTCAGGAGCTTCAGGTTT 780
QY 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA 840
QY 841 TTTATGAATCATAAAACTGCAACAGCAACTCGAATTCCTCGTGACCAAGCTTTTGG 900
Db 841 TTTATGAATCATAAAACTGCAACAGCAACTCGAATTCCTCGTGACCAAGCTTTTGG 900
QY 901 ACACCGGTGTGTGATCAGATGCAAGCGTGGGAAAGTTTTCATGCTACCCCGCTG 960
Db 901 ACACCGGTGTGTGATCAGATGCAAGCGTGGGAAAGTTTTCATGCTACCCCGCTG 960
QY 961 TGATGCGTGTGATGCAAGGACACGCAACCAATGGAATTCGTGTGAAAGTGGCCACT 1020
Db 961 TGATGCGTGTGATGCAAGGACACGCAACCAATGGAATTCGTGTGAAAGTGGCCACT 1020
QY 1021 TGGAGGAAACAAAGTGTCTCAAGAGACATGTTAGGATAGCAGGTCTTTGCAACCAAG 1080
Db 1021 TGGAGGAAACAAAGTGTCTCAAGAGACATGTTAGGATAGCAGGTCTTTGCAACCAAG 1080
QY 1081 ATGACACAGCTGTGTCAGATAGGCAATGCTAGTAATCTTTGGCCATGATGGAAG 1140
Db 1081 ATGACACAGCTGTGTCAGATAGGCAATGCTAGTAATCTTTGGCCATGATGGAAG 1140
QY 1141 GGCATCTCTCCACAAAGAGAAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTTA 1200
Db 1141 GGCATCTCTCCACAAAGAGAAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTTA 1200
QY 1201 AGTCAGCTGTGAAGACACCTTTGTAGTGAATTCAGTGAAGTGGGTGGAAATGACT 1260
Db 1201 AGTCAGCTGTGAAGACACCTTTGTAGTGAATTCAGTGAAGTGGGTGGAAATGACT 1260
QY 1261 GGATGTGCTCCCGCGGATCAGCTTTTATCGCCAGGAAATGCCCTTTCTC 1320
Db 1261 GGATGTGCTCCCGCGGATCAGCTTTTATCGCCAGGAAATGCCCTTTCTC 1320
QY 1321 TGGCTGATCATCTGAACCTCACTAATCATGCAATGTTGTCAGAGTTGTCATCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCACTAATCATGCAATGTTGTCAGAGTTGTCATCTGTTA 1380
QY 1381 ACTCTAAGATTCCTAAGGATGCTGTGTCGCGACAACTCAGTCTATCTGATGCTGT 1440
Db 1381 ACTCTAAGATTCCTAAGGATGCTGTGTCGCGACAACTCAGTCTATCTGATGCTGT 1440
QY 1441 ACCTTGAAGAGATGAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGTT 1500
Db 1441 ACCTTGAAGAGATGAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGTT 1500
QY 1501 GTGGGTGTGCTAGTACGAAAAATTAATACATAAATATATATATA 1547

Db 1501 GTGGGTGTGCTAGTACGAAAAATTAATACATAAATATATATATA 1547

RESULT 6
ACF05920

ID ACF05920 standard; cDNA; 1547 BP.

XX ACF05920;

XX 04-DEC-2003 (first entry)

XX Human bone morphogenic protein 2A polynucleotide.

XX Bone morphogenic protein 2A; BMP-2A; human; glaucoma; diagnosis; therapy;
XX ophthalmological; gene; ss.

XX Homo sapiens.

FH Key Location/Qualifiers
CDS 324..1514

FT /*tag= a

FT /product= "BMP-2A"

XX WO2003055443-A2.

XX 10-JUL-2003.

XX 31-OCT-2002; 2002WO-US035251.

XX 31-OCT-2001; 2001US-0334852P.

XX (ALCO-) ALCON INC.
XX (UNT-) UNIV NORTH TEXAS HEALTH SCI CENT.

XX Clark AF, Wordinger RJ;

XX WPI; 2003-559253/52.

XX P-PSDB; ABR62824.

XX Diagnosing glaucoma in a sample comprises detecting altered expression of
XX bone morphogenic proteins in sample from a cell or bodily fluid.

XX Claim 1; Fig 1a-c; 55pp; English.

XX The present sequence is a nucleotide sequence for human bone morphogenic
XX protein 2A (BMP-2A). RT-PCR showed BMP-2 to be expressed in the human
XX trabecular meshwork and optic nerve head. A claimed method for diagnosing
XX glaucoma involves detecting altered expression of a BMP family member
XX such as BMP-2A by PCR in a sample obtained e.g. from blood or buccal
XX cells. Primers used in the PCR may comprise contiguous nucleotides of the
XX present sequence. A claimed method for treating glaucoma comprises
XX administering an agonist of BMP-2, BMP-4, BMP-5, BMP-7 or Smad 1/5, or an
XX antagonist of chordin, gremlin or follistatin. A claimed method of
XX identifying a therapeutic agent for treatment of glaucoma comprises
XX identifying a substance that inhibits or stimulates BMP-induced Smad
XX signalling pathways or BMP-regulated gene expression, using recombinant
XX cells expressing BMP-2A, BMP-4, BMP-5 or BMP-7

XX Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Query Match 100.0%; Score 1547; DB 10; Length 1547;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTCTTGAACCTTCAGGAGAAATACTTGGCAGCCCACTTTGGCGGCGGCTT 60

Db 1 GGGGACTTCTTGAACCTTCAGGAGAAATACTTGGCAGCCCACTTTGGCGGCGGCTT 60

QY 61 TGCCCCAGGAGGCTGCTTCCCATCTCCGAGCCCAACCGCCCTCCACTCTCTGGGCT 120

Db 61 TGCCCCAGGAGGCTGCTTCCCATCTCCGAGCCCAACCGCCCTCCACTCTCTGGGCT 120

121 TGCCCGACACTGAGACGCTGTTCACAGCTGAAAGAGAGAGACTCGCGCGCGGCACCCGG 180
121 TGCCCGACACTGAGACGCTGTTCACAGCTGAAAGAGAGAGACTCGCGCGCGGCACCCGG 180
181 GAGAAGGAGGAGGCAAGAAAGAAAGGAAACGGAATTCGGTCTTTCGCCAGAGTCTTTGACC 240
181 GAGAAGGAGGAGGCAAGAAAGAAAGGAAACGGAATTCGGTCTTTCGCCAGAGTCTTTGACC 240
241 AGAGTTTTTCCATGTGAGACGCTCTTTCAAATGGAAGCTGTCCCGCGTGTCTTTAGACGGA 300
241 AGAGTTTTTCCATGTGAGACGCTCTTTCAAATGGAAGCTGTCCCGCGTGTCTTTAGACGGA 300
301 CTGCGGTCTCTCTAAAGGTTCACATGTTGGCGCGGACCCCGTGTCTTCTAGCGTTGCTGC 360
301 CTGCGGTCTCTCTAAAGGTTCACATGTTGGCGCGGACCCCGTGTCTTCTAGCGTTGCTGC 360
361 TTCCCCAGGTCCTCTCTGCGCGCGCGGCTGGCCCTCGTTCCGAGCTGGCGCGCAGGAAGT 420
421 TCGCGCGCGGTCGTTCGCGCGCGCGGCTGGCCCTCGTTCCGAGCTGGCGCGCAGGAAGT 420
421 TCGCGCGCGGTCGTTCGCGCGCGCGGCTGGCCCTCGTTCCGAGCTGGCGCGCAGGAAGT 480
481 TCGAGTTTCGCGCTCTCAGCATGTTTCGCGCTGAAACAGAGACCCACCCAGCAGGAGACG 540
481 TCGAGTTTCGCGCTCTCAGCATGTTTCGCGCTGAAACAGAGACCCACCCAGCAGGAGACG 540
541 CCGTGGTGCCTCTCTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAGCGCGGCTCAC 600
541 CCGTGGTGCCTCTCTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAGCGCGGCTCAC 600
601 CCGCGCCAGACACCGGTTGAGAGAGGAGCGAGCCAGCGGACCAACACTGTGGCGAGCTTCC 660
601 CCGCGCCAGACACCGGTTGAGAGAGGAGCGAGCCAGCGGACCAACACTGTGGCGAGCTTCC 660
661 ACCATGAAGATCTTTGGAGAACTACCAAGAAACGAGTGGGAAACAAACCCGAGATTCT 720
661 ACCATGAAGATCTTTGGAGAACTACCAAGAAACGAGTGGGAAACAAACCCGAGATTCT 720
721 TCTTTAAATTAAGTTCTATCCCAACGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTT 780
721 TCTTTAAATTAAGTTCTATCCCAACGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTT 780
781 TCCGAGACAGATCAAGATCTTTAGGAACCAATAGCAGTTTCCATCACCAGATTAAATA 840
781 TCCGAGACAGATCAAGATCTTTAGGAACCAATAGCAGTTTCCATCACCAGATTAAATA 840
841 TTTATGAATCATAAACCTGCAACAGCCAACTCGAAATTCCTGACAGACTTTTGG 900
841 TTTATGAATCATAAACCTGCAACAGCCAACTCGAAATTCCTGACAGACTTTTGG 900
901 ACACAGGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 960
901 ACACAGGTTGGTGAATCAGAAATCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 960
961 TGATCGGTGACGTGCACAGGGAACGCAACCAATGATTCGTTGGTGAAGTGGCCACT 1020
961 TGATCGGTGACGTGCACAGGGAACGCAACCAATGATTCGTTGGTGAAGTGGCCACT 1020
1021 TGGAGGAGAAACAAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAG 1080
1021 TGGAGGAGAAACAAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAG 1080
1081 ATGAACACAGCTGGTTCACAGATAAGGCCATTTGCTAGTAACTTTGGCCATGATGGAAG 1140
1081 ATGAACACAGCTGGTTCACAGATAAGGCCATTTGCTAGTAACTTTGGCCATGATGGAAG 1140
1141 GGCATCTCTCCAAAGAGAGAAACGTCAGGCCAAACACAAACAGCGGAAACGCCTTA 1200
1141 GGCATCTCTCCAAAGAGAGAAACGTCAGGCCAAACACAAACAGCGGAAACGCCTTA 1200
1201 AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGTGGAATGACT 1260

Db 1201 AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGACTTCAGTGAGCTGGGTGGATGACT 1260
Qy 1261 GGAATGTGGTCCCGCGGGTATCAACGCTTTTATCTGCCACGAGAAATGCCCTTTTCCTC 1320
Db 1261 GGAATGTGGTCCCGCGGGTATCAACGCTTTTATCTGCCACGAGAAATGCCCTTTTCCTC 1320
Qy 1321 TGGCTGATCATCTGAACCTCCACTAAATCATGCCATTTGTTTCAGAGCTTGGTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCCACTAAATCATGCCATTTGTTTCAGAGCTTGGTCAACTCTGTTA 1380
Qy 1381 ACTCTAAGATTTCTTAAGCGCATGCTGTCTCCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTTCTTAAGCGCATGCTGTCTCCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGAAATGAAAAGGTTGTTATTAAGAACTATCAGGACATGCTGTGAGGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAAAGGTTGTTATTAAGAACTATCAGGACATGCTGTGAGGGTT 1500
Qy 1501 GTGGGTGTGCTAGTACAGCAAAATTAATAACATATAATATATATA 1547
Db 1501 GTGGGTGTGCTAGTACAGCAAAATTAATAACATATAATATATA 1547

RESULT 7
ADD14609
ID ADD14609 standard; cDNA; 1547 BP.
XX
AC ADD14609;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human src biomarker polynucleotide SEQ ID NO:3.
XX
KW predictor set; protein tyrosine kinase activity modulator;
KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
KW gene therapy; drug sensitivity; genetic profile; cancer; human; gene; ss.
XX Homo sapiens.
XX WO2003062395-A2.
XX
PD 31-JUL-2003.
XX
PF 17-JAN-2003; 2003WO-US001981.
XX
PR 18-JAN-2002; 2002US-0350061P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Huang F, Fairchild CR, Lee FY, Shaw P;
XX
XX WPI; 2003-636735/60.
XX
XX P-PSDB; ADD14015.
XX
XX New polynucleotides and polypeptides for predicting the activity of
XX compounds that interact with protein tyrosine kinases and/or protein
XX tyrosine kinase pathways.
XX
XX Claim 2; SEQ ID NO 3; 139pp; English.
XX
XX The present invention describes a predictor set comprising a plurality of
XX polynucleotides or polypeptides whose expression pattern is predictive of
XX the response of cells to treatment with a compound that modulates protein
XX tyrosine kinase activity or members of the protein tyrosine kinase
XX pathway. Also described: (1) predicting whether a compound is capable of
XX modulating the activity of cells, comprising obtaining a sample of cells,
XX determining whether the cells express a plurality of markers, and
XX correlating the expression of the markers to the compound's ability to
XX modulate the activity of the cells; (2) a plurality of cell lines for
XX identifying polynucleotides and polypeptides whose expression levels
XX correlate with compound sensitivity or resistance of cells associated
XX with a disease state; and (3) identifying polynucleotides and

CC polypeptides that predict compound sensitivity or resistance of cells
CC associated with a disease state, comprising subjecting the plurality of
CC cell lines to one or more compounds, analysing the expression pattern of
CC a microarray of polynucleotides or polypeptides, and selecting
CC polynucleotides or polypeptides that predict the sensitivity or
CC resistance of cells associated with a disease state by using the
CC expression pattern of the microarray. The polynucleotides and
CC polypeptides have cytostatic activities, and can be used in gene therapy.
CC The polynucleotides and polypeptides are useful in predicting the
CC activity of compounds that interact with protein tyrosine kinases and/or
CC protein tyrosine kinase pathways. These may be used in determining drug
CC sensitivity in patients to allow the development of individualized
CC genetic profiles which aid in treating diseases and disorders (e.g.
CC cancer) based on patient response at a molecular level. The present
CC sequence is used in the exemplification of the present invention.

XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Query Match 100.0%; Score 1547; DB 10; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTTGAACCTTGCAGGAGAGATAAATTGCGCACCCACCTTTGGCGCGGTGCCTT 60
DB 1 GGGGACTTTTGAACCTTGCAGGAGAGATAAATTGCGCACCCACCTTTGGCGCGGTGCCTT 60
QY 61 TGCCCCAGCGGAGCTGCTTCCGACATCTCCGAGCCCGCCGCTCCACTCTCCGCGCT 120
DB 61 TGCCCCAGCGGAGCTGCTTCCGACATCTCCGAGCCCGCCGCTCCACTCTCCGCGCT 120
QY 121 TGCCCCGACA CTGAGACGCTGTTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGGACCCGG 180
DB 121 TGCCCCGACA CTGAGACGCTGTTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGGACCCGG 180
QY 181 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
DB 181 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 241 AGAGTTTTTCCATGTTGAGAGCTCTTTCAATGAGAGCTGTCGCGGCTCTTCTTAGACGA 300
DB 241 AGAGTTTTTCCATGTTGAGAGCTCTTTCAATGAGAGCTGTCGCGGCTCTTCTTAGACGA 300
QY 301 CTGCGGCTCTCTTAAAGGTGACATGTTGGCGGAGCCCGCTGCTTCTTAGGTTGCTGC 360
DB 301 CTGCGGCTCTCTTAAAGGTGACATGTTGGCGGAGCCCGCTGCTTCTTAGGTTGCTGC 360
QY 361 TTCCCCAGGTCTCTCTGCGCGCGGCTGCGCTCTGTTCCGAGCTGCGCGGAGGAGT 420
DB 361 TTCCCCAGGTCTCTCTGCGCGCGGCTGCGCTCTGTTCCGAGCTGCGCGGAGGAGT 420
QY 421 TCGCGGCGGCTGCTGCGGCGCGGCTCTCTGAGGCTGCTGAGGCTGCTGAGGAGT 480
DB 421 TCGCGGCGGCTGCTGCGGCGCGGCTCTCTGAGGCTGCTGAGGCTGCTGAGGAGT 480
QY 481 TCGAGTTGCGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGAGT 540
DB 481 TCGAGTTGCGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGAGT 540
QY 541 CGGTGGTGGCCCCCTTACATGCTAGACCTGATCGCAGGCACTCAGGTGAGGCTGCTGAG 600
DB 541 CGGTGGTGGCCCCCTTACATGCTAGACCTGATCGCAGGCACTCAGGTGAGGCTGCTGAG 600
QY 601 CGGCCCCAGACCAACCGGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 601 CGGCCCCAGACCAACCGGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 ACCATGAGAGATCTTTGGAAGAACTACACAGAAACGAGTGGGAGGAGGAGGAGGAGGAGTCT 720
DB 661 ACCATGAGAGATCTTTGGAAGAACTACACAGAAACGAGTGGGAGGAGGAGGAGGAGGAGTCT 720
QY 721 TCTTTAAATTAAGTTCTATFCCCCAGGAGGAGTATATCACTCAGCAGAGCTTCAGGTTT 780
DB 721 TCTTTAAATTAAGTTCTATFCCCCAGGAGGAGTATATCACTCAGCAGAGCTTCAGGTTT 780

QY 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAAAAATAGCAGTTTCCATCACCGAATTAATA 840
DB 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAAAAATAGCAGTTTCCATCACCGAATTAATA 840
QY 841 TTTATGAATCATATAAACCTCAACAGCAACTCGAAATTCCTGACACAGACTTTTGG 900
DB 841 TTTATGAATCATATAAACCTCAACAGCAACTCGAAATTCCTGACACAGACTTTTGG 900
QY 901 ACACCGGTTGGTGAATCAGATGCAAGCAGGTGGAAAGTTTTCATGTCACCCCGCTG 960
DB 901 ACACCGGTTGGTGAATCAGATGCAAGCAGGTGGAAAGTTTTCATGTCACCCCGCTG 960
QY 961 TGATGCGGTGACCTGACAGGAGACAGCCAACTGGAATTCGTGCTGGAAGTGGCCACT 1020
DB 961 TGATGCGGTGACCTGACAGGAGACAGCCAACTGGAATTCGTGCTGGAAGTGGCCACT 1020
QY 1021 TGGAGGAGAAAACAAAGTGTCTTCAAGAGACATGTTAGGATAAGCAGGTCTTTGCAACCAAG 1080
DB 1021 TGGAGGAGAAAACAAAGTGTCTTCAAGAGACATGTTAGGATAAGCAGGTCTTTGCAACCAAG 1080
QY 1081 ATGAACACAGCTGCTGACAGATTAAGCCATTTGCTAGTAACTTTTGGCCATGATGGAAG 1140
DB 1081 ATGAACACAGCTGCTGACAGATTAAGCCATTTGCTAGTAACTTTTGGCCATGATGGAAG 1140
QY 1141 GGCATCTCTTCCACAAAAGAGAAAAAAGCTCAAGCCAAAACACAAAACAGGGAACCGCTTTA 1200
DB 1141 GGCATCTCTTCCACAAAAGAGAAAAAAGCTCAAGCCAAAACACAAAACAGGGAACCGCTTTA 1200
QY 1201 AGTCAGCTGTAAGAGACACACCTTTTGTAGTGAATTCAGTGACCTGGGGTGGAAATGACT 1260
DB 1201 AGTCAGCTGTAAGAGACACACCTTTTGTAGTGAATTCAGTGACCTGGGGTGGAAATGACT 1260
QY 1261 GGATTTGGTCTCCCCCGGGGTATCAGGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1320
DB 1261 GGATTTGGTCTCCCCCGGGGTATCAGGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1320
QY 1321 TGGCTGATCATCTGAACTCCCAATATCATGCTGATGTTTTCAGACGTTGGTCAACTCTGTTA 1380
DB 1321 TGGCTGATCATCTGAACTCCCAATATCATGCTGATGTTTTCAGACGTTGGTCAACTCTGTTA 1380
QY 1381 ACTTAAGATTCCTAAGGCACTGCTGTGTCGCGACAGAACTCAGTCTATCTCGATGCTGT 1440
DB 1381 ACTTAAGATTCCTAAGGCACTGCTGTGTCGCGACAGAACTCAGTCTATCTCGATGCTGT 1440
QY 1441 ACCTTGACGAGATGAAAAAGGTGTTATTAAGAACTATCAGGACATGTTGTTGGAGGTT 1500
DB 1441 ACCTTGACGAGATGAAAAAGGTGTTATTAAGAACTATCAGGACATGTTGTTGGAGGTT 1500
QY 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAATACATAAATATATATA 1547
DB 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAATACATAAATATATATA 1547

RESULT 8

ID ADE85186 standard; DNA; 1547 BP.

XX ADE85186;

XX AC ADE85186;

XX DT 29-JAN-2004 (first entry)

XX DE Farnesyl transferase inhibitor modulated leukemia associated gene #405.

XX KW ss; cytostatic; farnesyl transferase inhibitor; gene expression;

XX OS quinolone; leukemia; cancer.

XX OS Homo sapiens.

XX FN WO2003038129-A2.

XX PD 08-MAY-2003.

XX XX

PF 30-OCT-2002; 2002WO-US034784.
XX
PR 30-OCT-2001; 2001US-0338997P.
PR 30-OCT-2001; 2001US-0340081P.
PR 30-OCT-2001; 2001US-0340938P.
PR 30-OCT-2001; 2001US-0341012P.
XX
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Raponi M;
XX
XX WPI; 2003-513497/48.
XX
XX
PT Determining whether a patient will respond to treatment with a farnesyl
PT transferase inhibitor, by analyzing the expression of gene that is
PT differentially modulated in the presence of the inhibitor.
XX
XX Disclosure; SEQ ID NO 405; 346pp; English.
XX
XX The invention relates to a method of determining whether a patient will
CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC analyzing the expression of gene that is differentially modulated in the
CC presence of an FTI. The method is useful for determining whether a
CC patient will respond to treatment with a FTI such as (B)-6-[amino(4-
CC chlorophenyl)](1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-
CC methyl-2-(1H)quinoline, monitoring the therapy of a patient, creating a
CC patient with leukemia with FTI if the analysis indicates that the patient
CC will respond. This sequence corresponds to a gene whose expression may be
CC modulated in the presence of FTI.
XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Query Match 100.0%; Score 1547; DB 10; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTCTTGAACCTTCAGGGAGNATACTTGGGACCCCACTTTGGCGGGTGCTT 60
DB 1 GGGGACTCTTGAACCTTCAGGGAGNATACTTGGGACCCCACTTTGGCGGGTGCTT 60
QY 61 TGCCCCGAGGAGCTGCTTCCGATCTCCGAGCCCAACCCGCTTCCACTCTCTGGGCT 120
DB 61 TGCCCCGAGGAGCTGCTTCCGATCTCCGAGCCCAACCCGCTTCCACTCTCTGGGCT 120
QY 121 TGCCCGACACTGAGACGCTGTTCCAGCTGAAAGAGAGACTGCGGGCCGACCCGG 180
DB 121 TGCCCGACACTGAGACGCTGTTCCAGCTGAAAGAGAGACTGCGGGCCGACCCGG 180
QY 181 GAGAGGAGGAGGCAAGAAAGGACGCAATTCGGTCTTGGCCAGGCTCTTTGACC 240
DB 181 GAGAGGAGGAGGCAAGAAAGGACGCAATTCGGTCTTGGCCAGGCTCTTTGACC 240
QY 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGGAGCTGTCCCGGCTGCTTTAGACGGA 300
DB 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGGAGCTGTCCCGGCTGCTTTAGACGGA 300
QY 301 CTGCGGCTCTCTAAGGTCGACATGCTGGGCGGGAACCCGCTGCTTCTAGCGTGTGC 360
DB 301 CTGCGGCTCTCTAAGGTCGACATGCTGGGCGGGAACCCGCTGCTTCTAGCGTGTGC 360
QY 361 TTCCCGAGGCTCTCTGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 TTCCCGAGGCTCTCTGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 TCGGCGGCGGCTGCTGCGGCGGCGGCTCATCTCCAGCCCTCTGACGAGGTCTGACGAGT 480
DB 421 TCGGCGGCGGCTGCTGCGGCGGCGGCTCATCTCCAGCCCTCTGACGAGGTCTGACGAGT 480
QY 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTGAAACAGAGACCCACCCCGAGGAGCG 540
DB 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTGAAACAGAGACCCACCCCGAGGAGCG 540
QY 541 CCGTGGTGCCCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAGCGCGGCTCAC 600

DB 541 CCGTGGTGCCCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTCAGCGGGCTCAC 600
QY 601 CCGCCCCAGACCAACCGGTTGGAGAGGCGCAGCCAGCGGCAACACTGTGTGGCGAGTTCC 660
DB 601 CCGCCCCAGACCAACCGGTTGGAGAGGCGCAGCCAGCGGCAACACTGTGTGGCGAGTTCC 660
QY 661 ACCATGAAGATCTTTGGAGAACTACAGAAACGAGTGGGAAAAACAACCCGGAGATTCT 720
DB 661 ACCATGAAGATCTTTGGAGAACTACAGAAACGAGTGGGAAAAACAACCCGGAGATTCT 720
QY 721 TCTTTAAATTTAAGTTCTATCCCGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTT 780
DB 721 TCTTTAAATTTAAGTTCTATCCCGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTT 780
QY 781 TCCGAGAACAGATGCAAGATGCTTTTAGGAAACAATAGCAGTTTCCATCACCGAATTATA 840
DB 781 TCCGAGAACAGATGCAAGATGCTTTTAGGAAACAATAGCAGTTTCCATCACCGAATTATA 840
QY 841 TTTATGAATCATFAAAACCTGCAACAGCCAACTCGAAATTTCCCGTGACAGACTTTTGG 900
DB 841 TTTATGAATCATFAAAACCTGCAACAGCCAACTCGAAATTTCCCGTGACAGACTTTTGG 900
QY 901 ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTGTGTACCCCGCTG 960
DB 901 ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTGTGTACCCCGCTG 960
QY 961 TGATCGGCTGACCTGCAAGGAGCAACGCAACCACTGATTCGTTGGTGGAGTGGCCACT 1020
DB 961 TGATCGGCTGACCTGCAAGGAGCAACGCAACCACTGATTCGTTGGTGGAGTGGCCACT 1020
QY 1021 TGGAGGAGAAACAAGGTGTTCTCAAGAGACATGTTAGGATAGCAGGTCTTTGACCAAG 1080
DB 1021 TGGAGGAGAAACAAGGTGTTCTCAAGAGACATGTTAGGATAGCAGGTCTTTGACCAAG 1080
QY 1081 ATGAACACAGCTGCTCAGATAAGGCAATGCTAGTAACTTTTGGCCATCATGAGAAAG 1140
DB 1081 ATGAACACAGCTGCTCAGATAAGGCAATGCTAGTAACTTTTGGCCATCATGAGAAAG 1140
QY 1141 GGCATCTCTCCAACAAGAGAAAAAGTCAAGCAACAACAACAGCGGAAACGCTTTA 1200
DB 1141 GGCATCTCTCCAACAAGAGAAAAAGTCAAGCAACAACAACAGCGGAAACGCTTTA 1200
QY 1201 AGTCAGGTGAAGAGACACCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACT 1260
DB 1201 AGTCAGGTGAAGAGACACCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACT 1260
QY 1261 GGATTTGGCTCCCGGGGTATCAGCGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1320
DB 1261 GGATTTGGCTCCCGGGGTATCAGCGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1320
QY 1321 TGGCTGATCATCTGAACCTCAATCATGCAATGTTGTGACAGTGGTCAACTCTGTTA 1380
DB 1321 TGGCTGATCATCTGAACCTCAATCATGCAATGTTGTGACAGTGGTCAACTCTGTTA 1380
QY 1381 ACTCTAAGATCTTAAGCATGCTGTGTCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
DB 1381 ACTCTAAGATCTTAAGCATGCTGTGTCCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
QY 1441 ACCTTGACGAGATGAAAGGTTGTTATTAAGAACTATCAGGACATGTTGTGGAGGTT 1500
DB 1441 ACCTTGACGAGATGAAAGGTTGTTATTAAGAACTATCAGGACATGTTGTGGAGGTT 1500
QY 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAATATAATATATATA 1547
DB 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAATATAATATATA 1547

RESULT 9
AAD63420
ID AAD63420 standard; DNA; 1547 BP.
XX
AC AAD63420;

XX	12-FEB-2004	(first entry)
DT		
XX		
DE	Human bone morphogenetic protein (BMP)-2 DNA.	
XX		
KW	Human; BMP; bone morphogenetic protein; cancer; therapy; gene; ds.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
CDS	324..1514	
FT	/*tag= a	
FT	/product= "Human BMP-2 protein"	
FT	324..1169	
FT	/*tag= b	
FT	/label= Signal_peptide	
FT	429..1127	
FT	/*tag= d	
FT	/note= "Transforming growth factor (TGF)-beta propeptide region"	
FT	replace(432,G)	
FT	/*tag= e	
FT	replace(584,G)	
FT	/*tag= f	
FT	replace(893,T)	
FT	/*tag= g	
FT	1170..1511	
FT	/*tag= c	
FT	/product= "Mature human BMP-2 protein"	
FT	1209..1511	
FT	/*tag= h	
FT	/note= "Transforming growth factor (TGF)-beta-like domain"	
XX		
PX	US2003134790-A1.	
PN		
XX	17-JUL-2003.	
PD		
XX		
XX	02-MAY-2002; 2002US-00139814.	
PP		
XX		
PR	11-JAN-2002; 2002US-00044716.	
XX		
XX	(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.	
PA		
XX	Langenfeld J;	
PI		
XX		
XX	WPI: 2003-829645/77.	
DR	P-PSDB; ABW01849.	
DR		
XX		
PT	Treating cancer, e.g. carcinoma of the breast, bladder, colon, kidney,	
PT	lung, ovary, thyroid, endometrium, omental, testis or liver, comprises	
PT	administering to the patient a bone morphogenetic protein-4 activity	
PT	inhibitor.	
XX		
XX	Disclosure; Page 15-17; 64pp; English.	
PS		
XX		
CC	The present invention relates to the use of BMP (bone morphogenetic	
CC	protein)-2 and BMP-4 used in treating cancer. The invention is useful for	
CC	treating cancer, e.g. carcinoma of the breast, bladder, colon, lung,	
CC	kidney, ovary, thyroid, endometrium, omental, testis and liver. The	
CC	present sequence is human bone morphogenetic protein (BMP)-2 DNA	
XX		
SQ	Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;	
Query Match	100.0%; Score 1547; DB 10; Length 1547;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1547; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GGCGACTTCCTTGAACCTTCAGGAGCAATAAATTCGGCACCCCACCTTTGGCGCGGTGCCCTT	60
Dd	1 GGCGACTTCCTTGAACCTTCAGGAGCAATAAATTCGGCACCCCACCTTTGGCGCGGTGCCCTT	60
Qy	61 TGCCCCCAGCGAGCGCTGCTTGCCCATCTCCGAGCCCCACC GCCCTCTCACTCTCTGGGCT	120

Db 1141 GGCACTCTCTCCACAAAGAGAAAAAGTCAAGCCAAACACAAACAGCGGAAACGCTTAA 1200
Qy 1201 AGTCAGCTGTAAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACT 1260
Db 1201 AGTCAGCTGTAAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACT 1260
Qy 1261 GGATTGTGGCTCCCGCGGGGTATCAGCGCTTTTACTGCCAGGAGAAATGCCCTTTTCTCTC 1320
Db 1261 GGATTGTGGCTCCCGCGGGGTATCAGCGCTTTTACTGCCAGGAGAAATGCCCTTTTCTCTC 1320
Qy 1321 TGGCTGATCACTGAACCTCCACTAATCATGTCATGTCATGTTGTCAGACGTGGTCAACTCTGTAA 1380
Db 1321 TGGCTGATCACTGAACCTCCACTAATCATGTCATGTCATGTTGTCAGACGTGGTCAACTCTGTAA 1380
Qy 1381 ACTCTAAGATTCCTAAGGCATGCTGTGCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTCCTAAGGCATGCTGTGCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGAAATGMAAAGGTGTATTAAAGAACTATCAGGACATGTTGTGGAGGGTT 1500
Db 1441 ACCTTGACGAGAAATGMAAAGGTGTATTAAAGAACTATCAGGACATGTTGTGGAGGGTT 1500
Qy 1501 GTGGGTGTGCTAGTACAGCAAAATTAATATACATAAATATATATA 1547
Db 1501 GTGGGTGTGCTAGTACAGCAAAATTAATATACATAAATATATATA 1547

RESULT 10
ABT17041
ID ABT17041 standard; DNA; 1547 BP.
XX
AC ABT17041;
XX
DT 03-APR-2003 (first entry)
XX
DE Human MP21 gene BMP2 SEQ ID No 15.
XX
KW Cytostatic; p21 pathway modulating agent; cancer; angiogenic; apoptotic;
KW cell proliferation disorder; MP21; gene; ds.
XX
OS Homo sapiens.
XX
FN WO2003006990-A1.
XX
PD 23-JAN-2003.
XX
PF 10-JUL-2002; 2002WO-US021549.
XX
PR 12-JUL-2001; 2001US-0305017P.
PR 10-OCT-2001; 2001US-0328491P.
PR 15-FEB-2002; 2002US-0357452P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Li D, Funke RP;
XX
DR WPI; 2003-221779/21.
DR P-PSDB; ABJ19767.
XX
PT Identifying candidate p21 pathway modulator, by contacting an assay
PT system having modifiers of p21 polypeptide or gene with a test agent to
PT provide a reference activity in system and detecting test agent-biased
PT activity.
XX
PS Example; Page 86-87; 199pp; English.
XX
CC The invention relates to a novel method for identifying a candidate p21
CC pathway modulating agent. The novel method comprises contacting an assay
CC system, comprising a purified MP21 polypeptide (modifier of p21) or
CC nucleic acid, with a test agent under conditions, so that but for the
CC presence of a test agent, the assay system provides a reference activity
CC and detection of test agent-biased activity of the assay system. The
CC novel method of the invention is useful for identifying a candidate p21

CC pathway modulating agent. The invention also includes a method for
CC modulating the p21 pathway of a cell, and a method for diagnosing a
CC disease e.g. cancer in a patient. The identified modulators are useful in
CC diagnosis, therapy and pharmaceutical development. The modulators are
CC useful in a variety of diagnostic and therapeutic applications including
CC angiogenic, apoptotic and cell proliferation disorders. This
CC polynucleotide sequence represents a gene encoding an MP21 protein of the
CC invention
XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Query Match 100.0%; Score 1547; DB 10; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTGAACCTTGCAGGGAGAAATACTTGGCAACCCCACTTTGGCGCGGTGCTT 60
Db 1 GGGGACTTCTTGAACCTTGCAGGGAGAAATACTTGGCAACCCCACTTTGGCGCGGTGCTT 60
Qy 61 TGGCCCAAGCGGAGCTTGTCCCATCTCCGAGCCCAACCGCCCTCCACTCCCTCGGCT 120
Db 61 TGGCCCAAGCGGAGCTTGTCCCATCTCCGAGCCCAACCGCCCTCCACTCCCTCGGCT 120
Qy 121 TGGCCCAAGCTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGGCGCGGCAACCGG 180
Db 121 TGGCCCAAGCTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGGCGCGGCAACCGG 180
Qy 181 GAGAAAGGAGGAGGCAAGAAAGAACGCAATTCGGTCTCTTGGCCCAAGGTCCTTTGACC 240
Db 181 GAGAAAGGAGGAGGCAAGAAAGAACGCAATTCGGTCTCTTGGCCCAAGGTCCTTTGACC 240
Qy 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGGAGCTGTCCCGCGTGTCTTTAGACGGA 300
Db 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGGAGCTGTCCCGCGTGTCTTTAGACGGA 300
Qy 301 CTGGGCTCTCTAAAGGTTCGACCATGTGGCGCGGACCCGCTGTCTTCTAGCGTTGCTGC 360
Db 301 CTGGGCTCTCTAAAGGTTCGACCATGTGGCGCGGACCCGCTGTCTTCTAGCGTTGCTGC 360
Qy 361 TTCCCAAGGTCTCTCTGGGCGGCGGCTGCGCTGCTTCCGAGCTGCGCGCGGCAAGT 420
Db 361 TTCCCAAGGTCTCTCTGGGCGGCGGCTGCGCTGCTTCCGAGCTGCGCGCGGCAAGT 420
Qy 421 TCGGCGGCGGCTGCTGCGGCGGCGGCTCATCCAGCCCTCTGAGAGCTCTGAGCGGAGT 480
Db 421 TCGGCGGCGGCTGCTGCGGCGGCGGCTCATCCAGCCCTCTGAGAGCTCTGAGCGGAGT 480
Qy 481 TCGAGTTGCGGCTGCTCAGCATGTTCGGCTTGAAACAGAGACCCACCCAGCAGGAGACG 540
Db 481 TCGAGTTGCGGCTGCTCAGCATGTTCGGCTTGAAACAGAGACCCACCCAGCAGGAGACG 540
Qy 541 CCGTGGTCCCGCTCATATGCTAGACCTGTATCGAGGCACTCAGGTGAGCGCGGCTCAC 600
Db 541 CCGTGGTCCCGCTCATATGCTAGACCTGTATCGAGGCACTCAGGTGAGCGCGGCTCAC 600
Qy 601 CCGCCCAAGACCAACCGGTTGGAGAGGCGGAGCCAGCCAGCCAACTGTGGCGAGCTTCC 660
Db 601 CCGCCCAAGACCAACCGGTTGGAGAGGCGGAGCCAGCCAGCCAACTGTGGCGAGCTTCC 660
Qy 661 ACCATGAAGAAATCTTTGGAAGAACTACAGAAACGAGTGGGAAACAAACCGGAGATTCT 720
Db 661 ACCATGAAGAAATCTTTGGAAGAACTACAGAAACGAGTGGGAAACAAACCGGAGATTCT 720
Qy 721 TCTTTAAATTTAAGTTCTATCCCAAGGAGGTTTATCAGCTCAGCAGAGCTTTCAGGTTT 780
Db 721 TCTTTAAATTTAAGTTCTATCCCAAGGAGGTTTATCAGCTCAGCAGAGCTTTCAGGTTT 780
Qy 781 TCCGAGACAGATCAGATGCTTTAGAAACATAGCAGTTTCCATCACCAGATTATA 840
Db 781 TCCGAGACAGATCAGATGCTTTAGAAACATAGCAGTTTCCATCACCAGATTATA 840
Qy 841 TTTATGAATCATATAAACCTTGCAACAGCCAACTCGAAATTCGCCGTGACCAAGCTTTGG 900
Db 841 TTTATGAATCATATAAACCTTGCAACAGCCAACTCGAAATTCGCCGTGACCAAGCTTTGG 900

Db 841 TTTATGAATCATAAACCTGCAACGACCACTCGAAATTCCTCCGTGACCACTTTTGG 900
Qy 901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTTCATGTACCCCGCGTG 960
Db 901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTTCATGTACCCCGCGTG 960
Qy 961 TGATCGGTGGACTGCACAGGACACGCCAACCATTGCTGTGGAGTGGCCACT 1020
Db 961 TGATCGGTGGACTGCACAGGACACGCCAACCATTGCTGTGGAGTGGCCACT 1020
Qy 1021 TGGAGGAGAAACAGGTGCTCCAGAGACATGTTAGGATAGCAGGTCTTTGACCAAG 1080
Db 1021 TGGAGGAGAAACAGGTGCTCCAGAGACATGTTAGGATAGCAGGTCTTTGACCAAG 1080
Qy 1081 ATGAACACAGCTGGTGCACAGATAAGGCCATTCTAGTAACCTTTTGGCCATGATGAAAG 1140
Db 1081 ATGAACACAGCTGGTGCACAGATAAGGCCATTCTAGTAACCTTTTGGCCATGATGAAAG 1140
Qy 1141 GGCATCCTCTCCACAAAGAGAAAAACGTCAGCCCAACACAAACAGCGGAAACGCTTA 1200
Db 1141 GGCATCCTCTCCACAAAGAGAAAAACGTCAGCCCAACACAAACAGCGGAAACGCTTA 1200
Qy 1201 AGTCAGCTGTGAAGACACCTTTGTAGTGGACTTCAGTGACGTGGGTGGAATGACT 1260
Db 1201 AGTCAGCTGTGAAGACACCTTTGTAGTGGACTTCAGTGACGTGGGTGGAATGACT 1260
Qy 1261 GGATTTGGCTCCCGGGGTATACAGCCTTTTACTGCCAGGAGATGCCCTTTTCCTC 1320
Db 1261 GGATTTGGCTCCCGGGGTATACAGCCTTTTACTGCCAGGAGATGCCCTTTTCCTC 1320
Qy 1321 TGGCTGATCATCTGAACCTCACTAATCATGCACTGTTTTCAGACGTTGGTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCACTAATCATGCACTGTTTTCAGACGTTGGTCAACTCTGTTA 1380
Qy 1381 ACTTAAGATTCCTAAGCATGCTGTGTCGCCAGACAACTAGTCTATCTCGATGCTGT 1440
Db 1381 ACTTAAGATTCCTAAGCATGCTGTGTCGCCAGACAACTAGTCTATCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGAAATGAAAGGTTGATTAAAGAACTATCAGACATGTTGGAGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAAGGTTGATTAAAGAACTATCAGACATGTTGGAGGTT 1500
Qy 1501 GTGGGTGCTGTAGTACAGCAAAATTAATATACATAAATATATATATA 1547
Db 1501 GTGGGTGCTGTAGTACAGCAAAATTAATATACATAAATATATATA 1547

RESULT 11
ADL13510
ID ADL13510 standard; DNA; 1547 BP.
XX
AC ADL13510;
XX
DT 06-MAY-2004 (first entry)
DE Osteoarthritis-associated polymorphic nucleotide #42.
XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
KW joint space narrowing; osteophyte development; joint pain;
KW osteoarthritis; SNP; single nucleotide polymorphism.
XX Homo sapiens.
XX WO2003054166-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US041225.
XX
PR 20-DEC-2001; 2001US-0342603P.
XX (INCY-) INCYTE GENOMICS INC.
XX

PI Jones KA, Schafer A;
XX
DR WPI; 2003-559141/52.
XX
PT Determining susceptibility of an individual to joint space narrowing,
osteophyte development and/or joint pain comprises identifying whether
the individual has at least one polymorphism in a polynucleotide encoding
a protein.
PT
XX
PS Disclosure; SEQ ID NO 42; 297pp; English.
XX
CC The invention relates to a method of determining susceptibility of an
individual to joint space narrowing and/or osteophyte development and/or
joint pain comprising identifying whether the individual has at least one
polymorphism in a polynucleotide encoding at least one of the protein
listed in the specification. The methods, composition and agent are
useful for modulating the susceptibility of an individual to joint space
narrowing and/or osteophyte development and/or joint pain that is
associated with a disease, preferably osteoarthritis. The cell line and
the non-human animal are useful for screening for an agent for diagnosing
an individual having susceptibility to joint space narrowing and/or
osteophyte development and/or joint pain. This sequence corresponds to
the polynucleotide encoding a protein listed in the specification. (Note:
The sequence data for this patent did not form part of the printed
specification but was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Query Match 100.0%; Score 1547; DB 10; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 TGCCCCAGCACTGAGACGCTGTTCCAGCGTGAAAGAGAGACTGCGCGCGGACCCGG 180
Qy 181 GAGAGGAGGAGGCAAGAAAAAGGAAACCGACATTCGGTCTTGGCCAGGTCTTTGACC 240
Db 181 GAGAGGAGGAGGCAAGAAAAAGGAAACCGACATTCGGTCTTGGCCAGGTCTTTGACC 240
Qy 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGGAGCTGTCCCGCGTGTCTTAGACCGA 300
Db 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGGAGCTGTCCCGCGTGTCTTAGACCGA 300
Qy 301 CTGCGGTCTCTAAAGGTCGACCATGTGTGGCGGACCGCTGTCTTAGCGTTGCTGC 360
Db 301 CTGCGGTCTCTAAAGGTCGACCATGTGTGGCGGACCGCTGTCTTAGCGTTGCTGC 360
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Db 361 TTCCCCAGGTCTCTTGGCGGCGGCTGCTGCTTCCGAGAGTGGCGCGCAGCAAGT 420
Qy 421 TCGGGCGGCGCTGCTGCGGGCGCCCTCATCCAGCCCTCTGACAGAGTCTTAGCGAGT 480
Db 421 TCGGGCGGCGCTGCTGCGGGCGCCCTCATCCAGCCCTCTGACAGAGTCTTAGCGAGT 480
Qy 481 TCGAGTTGCGGCTGCTCAGCATGTTTGGCCCTGAAACAGAGACCCACCCCGGAGCG 540
Db 481 TCGAGTTGCGGCTGCTCAGCATGTTTGGCCCTGAAACAGAGACCCACCCCGGAGCG 540
Qy 541 CCGTGGTGCCTTACATGCTAGACCTGTATCGAGGCACTCAGGTGAGCGGGCTCAC 600
Db 541 CCGTGGTGCCTTACATGCTAGACCTGTATCGAGGCACTCAGGTGAGCGGGCTCAC 600

[illegible]

RESULT 12

RESUL I.
ADN38841

ADN38841
ID ADN38841 standard; cDNA; 1547 BP.

AC ADN38841;

XX

DT 17-JUN-2004 (first entry)

XX

Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:159.

Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularization syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiac; immunomodulatory; vulnuary; gene therapy; vaccine; gene; ss.

Homo sapiens.

WO2003042661-A2.

22-MAY-2003

13-NOV-2002: 2002WO-US036810.

13-NOV-2001: 2001US-0350666P

13-NOV-2001; 2001US-0350666P;
21-NOV-2001; 2001US-0332464P;

21-NOV-2001; 2001US-032404F.
29-NOV-2001; 2001US-0334393P.

03-DEC-2001; 2001US-0335394P.

14-DEC-2001; 2001US-0340376P.

08-JAN-2002; 2002US-0347211P.

10-JAN-2002; 2002US-0347349P.

08-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0355250P.

13-FEB-2002; 2002US-0356714P.
20-FEB-2002; 2002US-0359077P

20-FEB-2002; 2002US-0359077P.
29-MAR-2002: 2002US-0368809P.

29-MAR-2002; 2002US-0368809P;
04-APR-2002; 2002US-0370110P;

04-APR-2002; 2002US-0370110F.
12-APR-2002; 2002US-0372246P.

05-JUN-2002; 2002US-0386614P.

16-JUL-2002; 2002US-0396839P.

22-JUL-2002; 2002US-0397775P.

22-JUL-2002; 2002US-0397845P.

09-SEP-2002; 2002US-0409450P.

(FOUO -) FOR PROTECTING OUR INFO

(EOSB-) EOS BIOTECHNOLOGY INC.

Afar D, Aziz N, Gingsburg WM, Gish KC, Glynn R, Hevezi PA;

Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A; Alar D, Aziz N, Gibburg NN, Giburg AC, Gyime N, H

WPI; 2003-468649/44.

P-PSDB; ADN38842.

Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.

Claim 8; SEQ ID NO 159; 1385pp; English.

The invention relates to nucleic acids and proteins (ADN38693-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularisation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a nucleic acid sequence of the invention.

Sequence 1547 BP: 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Query Match

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Best Local Similarity	100.00%; Pred. No. 0;

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PI Young PE, Ruben SM;
XX WPI; 2004-022075/02.
DR P-PSDB; ADH11579.
XX
PT New bone morphogenic protein polypeptides and polynucleotides, useful for
PT diagnosing, preventing, treating or ameliorating a medical condition,
PT e.g. diabetes, dyslipidemia, hypertension, coronary artery disease or
PT neuropathy.
XX
PS Example 1; SEQ ID NO 10; 224pp; English.
XX
CC The invention relates to human bone morphogenic protein (BMP)
CC polypeptides and the polynucleotides encoding them. The invention also
CC relates to a method for limiting weight gain, suppressing appetite or
CC reducing fat mass, comprising administering to a mammalian subject a
CC therapeutic amount of a BMP polypeptide, and a method for increasing the
CC sensitivity of a cell to insulin or increasing glucose uptake by a cell,
CC comprising contacting the cell with a BMP polypeptide. The BMP
CC polypeptides and polynucleotides are useful for diagnosing a pathological
CC condition or a susceptibility to a pathological condition in a subject or
CC for preventing, treating or ameliorating a medical condition, e.g.
CC diabetes, insulin resistance, hyperglycaemia, hypertension, coronary
CC artery disease, renal failure, neuropathy, metabolic disorders, glucose
CC metabolism disorder, endocrine disorders, obesity, weight loss, liver
CC disorders, cartilage and bone growth disorders, inflammation or aberrant
CC cell growth such as liver cancer. The BMP polypeptides and
CC polynucleotides are also useful for regulating nutritional partitioning,
CC limiting weight gain, suppressing appetite, reducing fat mass, increasing
CC the sensitivity of a cell to insulin or increasing glucose uptake by a
CC cell. This sequence represents a human BMP polynucleotide of the
CC invention.
XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Query Match 100.0%; Score 1547; DB 12; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTGAAACAGAGACCCACCCGAGCGGACG 540
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Job time : 685 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 20:20:29 ; Search time 221 Seconds
(without alignments)
12442.932 Million cell updates/sec

Title: US-10-801-648-1

Perfect score: 1547

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1547	100.0	1547	9	5166058-3
5	1547	100.0	3526	3	US-09-976-594-11
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7	1545.4	99.9	1547	2	US-08-469-411-1
8	1545.4	99.9	1547	3	US-09-780-601A-1
9	1545.4	99.9	2185	3	US-09-949-016-4668
10	1543.8	99.8	1547	2	US-07-679-451-1
11	1227.2	79.3	1260	2	US-07-841-646-4
12	1227.2	79.3	1260	2	US-07-901-703-14
13	1227.2	79.3	1260	2	US-08-147-023-4
14	1227.2	79.3	1260	2	US-08-447-570-4
15	1227.2	79.3	1260	2	US-08-449-700-4
16	1227.2	79.3	1260	2	US-08-449-699A-4
17	1227.2	79.3	1260	3	US-09-148-925C-4
18	1227.2	79.3	1260	3	US-08-957-425-4
19	1227.2	79.3	1260	3	US-10-321-799-4
20	1227.2	79.3	1260	6	PCT-US93-05446-14
21	1045.2	67.6	1314	3	US-08-713-556F-39
22	896.6	58.0	1233	2	US-08-362-670B-27
23	896.6	58.0	1233	3	US-08-333-576C-27
24	896.6	58.0	1233	3	US-08-808-324-27

25	896.6	58.0	1233	3	US-09-945-182-27	Sequence 27, Appl
26	896.6	58.0	1233	6	PCT-US94-14030A-27	Sequence 27, Appl
27	880	56.9	14759	3	US-09-661-887-1	Sequence 1, Appl
28	878.4	56.8	15203	3	US-09-949-016-16410	Sequence 16410, A
29	681.2	44.0	15144	3	US-08-458-434A-6	Sequence 6, Appl
30	623.2	40.3	1992	2	US-08-455-550-6	Sequence 6, Appl
31	416.4	26.9	955	2	US-08-455-550-3	Sequence 7, Appl
32	385.4	24.9	1558	2	US-08-455-550-7	Sequence 7, Appl
33	378	24.4	406	3	US-08-868-452-35	Sequence 35, Appl
34	375	24.2	1751	2	US-08-377-292-4	Sequence 4, Appl
35	375	24.2	1788	2	US-07-841-646-6	Sequence 6, Appl
36	375	24.2	1788	2	US-07-901-703-18	Sequence 18, Appl
37	375	24.2	1788	2	US-08-147-023-6	Sequence 6, Appl
38	375	24.2	1788	2	US-08-447-570-6	Sequence 6, Appl
39	375	24.2	1788	2	US-08-449-699A-6	Sequence 6, Appl
40	375	24.2	1788	2	US-08-148-925C-6	Sequence 6, Appl
41	375	24.2	1788	3	US-08-957-425-6	Sequence 6, Appl
42	375	24.2	1788	3	US-10-321-799-6	Sequence 6, Appl
43	375	24.2	1788	3	US-10-321-799-6	Sequence 6, Appl
44	375	24.2	1788	6	PCT-US93-05446-18	Sequence 18, Appl
45	375	24.2	1945	3	US-09-949-016-1476	Sequence 1476, Ap

ALIGNMENTS

RESULT 1
US-08-377-292-2
; Sequence 2, Application US/08377292
; Patent No. 5693615
; GENERAL INFORMATION:
; APPLICANT: STONE, ROGER L.
; TITLE OF INVENTION: THERAPEUTIC FORMULAS FOR OSTEOINDUCTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: The Procter & Gamble Company
; STREET: 11810 East Miami River Road
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 45239-8707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,292
; FILING DATE: 23-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,435
; FILING DATE:
; APPLICATION NUMBER: US/08/117,367
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Corstange, Brahm J.
; REGISTRATION NUMBER: 34,804
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-245-2858
; TELEFAX: 513-741-3012
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1547 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-377-292-2

Query Match 100.0%; Score 1547; DB 2; Length 1547;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GGGCACTTCTTGAACTTTCAGGGAGAAATAA	CTTCGCA	CCCCACTTTTGGCGCGTGCCTT	60
Db	1	GGGCACTTCTTGAACTTTCAGGGAGAAATAA	CTTCGCA	CCCCACTTTTGGCGCGTGCCTT	60
Qy	61	TGCCCCAGCGGAGCTGTTCCGCACTCTCGAG	CCCCACCGCCCTCTCACTCTCGCGCT	120	
Db	61	TGCCCCAGCGGAGCTGTTCCGCACTCTCGAG	CCCCACCGCCCTCTCACTCTCGCGCT	120	
Qy	121	TGCCCCGACCTGAGACGCTGTTCCAGCGTGA	AAAGAGAGACTGCGCGCGCGCACCCGG	180	
Db	121	TGCCCCGACCTGAGACGCTGTTCCAGCGTGA	AAAGAGAGACTGCGCGCGCGCACCCGG	180	
Qy	181	GAGAAGGAGGAGGCAAAAGAAACGGA	CATTCCGTCCTTGTGCGCCAGGTCCTTTGACC	240	
Db	181	GAGAAGGAGGAGGCAAAAGAAAGAA	CGGACATTCCGTCCTTGTGCGCCAGGTCCTTTGACC	240	
Qy	241	AGAGTTTTTCATGTGAGACGCTCTTTCAATG	GACGTCGTCGCCGCTGCTTTTAGACGGA	300	
Db	241	AGAGTTTTTCATGTGAGACGCTCTTTCAATG	GACGTCGTCGCCGCTGCTTTTAGACGGA	300	
Qy	301	CTCGGGTCTCCTAAAGGTCGACATGTTGGC	CGGACCCGCTGCTTTTAGCGTTCGCTTCG	360	
Db	301	CTCGGGTCTCCTAAAGGTCGACATGTTGGC	CGGACCCGCTGCTTTTAGCGTTCGCTTCG	360	
Qy	361	TTCCCCAGGTCCTCTCGGGCGCGCTGCGCT	CGTTCGCGAGCTGGCGCGCAGGAAGT	420	
Db	361	TTCCCCAGGTCCTCTCGGGCGCGCGCTGCG	CTGCTCGTTCGCGAGCTGGCGCGCAGGAAGT	420	
Qy	421	TCGCGGCGGGTCGTCGCGGCGCGCCCTCAT	CCAGCCCTCTGACGAGTCTCTGAGCGAGT	480	
Db	421	TCGCGGCGGGTCGTCGCGGCGCGCCCTCAT	CCAGCCCTCTCTGACGAGTCTCTGAGCGAGT	480	
Qy	481	TCGAGTTTCGGCTGCTCAGCATGTTCCGGC	CTGAAACAGAGACCACCCCCAGCAGGACG	540	
Db	481	TCGAGTTTCGGCTGCTCAGCATGTTCCGGC	CTGAAACAGAGACCACCCCCAGCAGGACG	540	
Qy	541	CCGTGTGCCCCCTTACATGCTAGACCTGTAT	CCAGGCACTCAGGTCAGCCGGCTCAC	600	
Db	541	CCGTGTGCCCCCTTACATGCTAGACCTGTAT	CCAGGCACTCAGGTCAGCCGGCTCAC	600	
Qy	601	CCGCCCCAGACACCCGTTGGAGGGCAGCAG	CCGAGCCAACTGTGCGCAGCTTCC	660	
Db	601	CCGCCCCAGACACCCGTTGGAGGGCAGCAG	CCGAGCCAACTGTGCGCAGCTTCC	660	
Qy	661	ACCATGAGATCTTTGGAGAACTACAGAAAC	AGTGGGAAACAAACCGGAGTCT	720	
Db	661	ACCATGAGATCTTTGGAGAACTACAGAAAC	AGTGGGAAACAAACCGGAGTCT	720	
Qy	721	TCTTTAATTTAAGTCTTATCCCACGAGAGT	TTATACCTCAGCAGAGCTTCAGGTTT	780	
Db	721	TCTTTAATTTAAGTCTTATCCCACGAGAGT	TTATACCTCAGCAGAGCTTCAGGTTT	780	
Qy	781	TCCGAGAACAGATCAAGATGCTTTTAGGAAA	CAATAGCAGTTTCCATCACCGGAATTAATA	840	
Db	781	TCCGAGAACAGATCAAGATGCTTTTAGGAAA	CAATAGCAGTTTCCATCACCGGAATTAATA	840	
Qy	841	TTTATGAAATCATATAAACTCTGCAACG	CCAACTCGAAATTTCCCGTGACACAGACTTTTGG	900	
Db	841	TTTATGAAATCATATAAACTCTGCAACG	CCAACTCGAAATTTCCCGTGACACAGACTTTTGG	900	
Qy	901	ACACAGGTTGGTCAATCAGAACTCAAGC	AGGTGGGAAAGTTTTGATGTACCCCCCGCTG	960	
Db	901	ACACAGGTTGGTCAATCAGAACTCAAGC	AGGTGGGAAAGTTTTGATGTACCCCCCGCTG	960	
Qy	961	TGATGCGGTGGAAGTCTGCAAGGACACG	CGCAACCATGGAATTCGTGGTGGAAAGTGCCCACT	1020	
Db	961	TGATGCGGTGGAAGTCTGCAAGGACACG	CGCAACCATGGAATTCGTGGTGGAAAGTGCCCACT	1020	
Qy	1021	TGGAGGAGAAACAAGGTGTTCTCAAGAGA	CATGTTAGATAAGCAGGTCCTTTGCAACAAG	1080	
Db	1021	TGGAGGAGAAACAAGGTGTTCTCAAGAGA	CATGTTAGATAAGCAGGTCCTTTGCAACAAG	1080	

Qy		1081	ATGAACACAGCTGGTCA CAGATAAGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGAAG	1140
Db		1081	ATGAACACAGCTGGTCA CAGATAAGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGAAG	1140
Qy		1141	GGCATCTCTCCACA AAGAGAAAACGTCAAGCAGAAACACAACAACGCGAAGCGCTTGA	1200
Db		1141	GBCATCTCTCCACA AAGAGAAAACGTCAAGCAGAAACACAACAACGCGAAGCGCTTGA	1200
Qy		1201	AGTCAGCTGTAA GAGACACCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACT	1260
Db		1201	AGTCAGCTGTAA GAGACACCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACT	1260
Qy		1261	GGATTGGGCTCCCC CGGGGTATCAGCGCTTTTACTGCACCGAGAGATGCCCTTTTCCCTC	1320
Db		1261	GGATTGGGCTCCCC CGGGGTATCAGCGCTTTTACTGCACCGAGAGATGCCCTTTTCCCTC	1320
Qy		1321	TGGCTGATCATCTGA ACTCCAATAATCATGCCATTGTTCAGACGTTGGTCAA CTCTGTTA	1380
Db		1321	TGGCTGATCATCTGA ACTCCAATAATCATGCCATTGTTCAGACGTTGGTCAA CTCTGTTA	1380
Qy		1381	ACTCTAAGATTCTTA AGGCANGCTGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGT	1440
Db		1381	ACTCTAAGATTCTTA AGGCANGCTGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGT	1440
Qy		1441	ACCTTGACGAGAA TGAAGGTTGTATTAAAGAAACTATCAGGACATGGTTGTGCGAGGTT	1500
Db		1441	ACCTTGACGAGAA TGAAGGTTGTATTAAAGAAACTATCAGGACATGGTTGTGCGAGGTT	1500
Qy		1501	GTGGGTGTCCGTAGT ACAGCAAAATTAATAFACATAAATATATATATA	1547
Db		1501	GTGGGTGTCCGTAGT ACAGCAAAATTAATAFACATAAATATATATATA	1547

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RESULT 2
US-07-721-847A-3
; Sequence 3, Application US/07721847A
; Patent No. 6150328
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: No. 6150328el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/721,847A
; FILING DATE: 14-JUN-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: 5160C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-2OS
IMMEDIATE SOURCE:
LIBRARY: U2OS cDNA in Lambda GT10
CLONE: Lambda U2OS-39
POSITION IN GENOME:
UNITS: bp
FEATURE:
NAME/KEY: CDS
LOCATION: 356..1546
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1202..1543
FEATURE:
NAME/KEY: mRNA
LOCATION: 14..1607
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 356..424
US-07-721-847A-3
Query Match 100.0%; Score 1547; DB 3; Length 1607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGACTTCTTGAACTTGGCAGGAGAAATACTTGGCGACCCCACTTTGGCGCGGTGCTT 60
DB 33 GGGGACTTCTTGAACTTGGCAGGAGAAATACTTGGCGACCCCACTTTGGCGCGGTGCTT 92
QY 61 TGCCCGAGGGAGCGCTTGGCCATCTCCGAGCCCAACCGCCCTCCACTCTCGGCT 120
DB 93 TGCCCGAGGGAGCGCTTGGCCATCTCCGAGCCCAACCGCCCTCCACTCTCGGCT 152
QY 121 TGCCCGACACTGAGACGCTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGGACCCGG 180
DB 153 TGCCCGACACTGAGACGCTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGGACCCGG 212
QY 181 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 213 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 272
QY 241 AGAGTTTTCCATGTGGACGCTTTCAATGAGACGTGTCGCGCGCGGCTTCTTAGACGA 300
DB 273 AGAGTTTTCCATGTGGACGCTTTCAATGAGACGTGTCGCGCGCGGCTTCTTAGACGA 332
QY 301 CTGCGGCTCTCTTAAAGGTCGACCATGTTGGCGGAGACCGGCTGCTTCTAGCGTTGCTGC 360
DB 333 CTGCGGCTCTCTTAAAGGTCGACCATGTTGGCGGAGACCGGCTGCTTCTAGCGTTGCTGC 392
QY 361 TTCCCGAGGCTCTCTTGGCGCGCGGCTGCTTCTCGGAGCTGGGCGCGCAGGAGT 420
DB 393 TTCCCGAGGCTCTCTTGGCGCGCGGCTGCTTCTCGGAGCTGGGCGCGCAGGAGT 452
QY 421 TCGCGCGCGGCTGCTGCGCGCGCGGCTGCTTCCAGCGCTCTGACGAGTCTGACGAGT 480
DB 453 TCGCGCGCGGCTGCTGCGCGCGCGGCTGCTTCCAGCGCTCTGACGAGTCTGACGAGT 512
QY 481 TCGAGTTGCGGCTGCTGAGCATGTTGCGGCTGAAACAGAGACCCACCCCGCAGGAGG 540
DB 513 TCGAGTTGCGGCTGCTGAGCATGTTGCGGCTGAAACAGAGACCCACCCCGCAGGAGG 572
QY 541 CGGTGGTGCCTCCCTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGCTCAC 600
DB 573 CGGTGGTGCCTCCCTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGCTCAC 632
QY 601 CGGCCCCAGACACCGGTTGGAGAGGCGAGCGGAGGCGCAACTGTGCGCAGCTTCC 660
DB 633 CGGCCCCAGACACCGGTTGGAGAGGCGAGCGGAGGCGCAACTGTGCGCAGCTTCC 692

QY 661 ACCATGAAGAACTTTTGAAGAACTTACCCAGAAACGAGTGGGAAACAAACCCGAGATTCT 720
DB 693 ACCATGAAGAACTTTTGAAGAACTTACCCAGAAACGAGTGGGAAACAAACCCGAGATTCT 752
QY 721 TCTTTAATTTAAGTTCTATCCCAAGGAGGAGTTTATCACTCAGCAGAGCTTCAAGTTT 780
DB 753 TCTTTAATTTAAGTTCTATCCCAAGGAGGAGTTTATCACTCAGCAGAGCTTCAAGTTT 812
QY 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAAATTAATA 840
DB 813 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAAATTAATA 872
QY 841 TTTATGAATCATAAACCTGCAACAGCCAACTCCGATGCAAGACTTTTGG 900
DB 873 TTTATGAATCATAAACCTGCAACAGCCAACTCCGATGCAAGACTTTTGG 932
QY 901 ACACGAGTTGCTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 960
DB 933 ACACGAGTTGCTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 992
QY 961 TGATGCGGTGACTGCAAGGAGACAGCCAACTGCAAGTTCGTTGTTGGAAGTGGGCCACT 1020
DB 993 TGATGCGGTGACTGCAAGGAGACAGCCAACTGCAAGTTCGTTGTTGGAAGTGGGCCACT 1052
QY 1021 TGGAGGAGAAACAAGGTGCTTCCAGAGACATGTTAGGATAAGCAGGTCTTTGCAACCAAG 1080
DB 1053 TGGAGGAGAAACAAGGTGCTTCCAGAGACATGTTAGGATAAGCAGGTCTTTGCAACCAAG 1112
QY 1081 ATGAACACAGCTGGTCAAGATAGGCCATTTCTAGTAACTTTTGGCCATGATGGAAG 1140
DB 1113 ATGAACACAGCTGGTCAAGATAGGCCATTTCTAGTAACTTTTGGCCATGATGGAAG 1172
QY 1141 GGCATCTCTCCACAAAAGAGAAAACGTCAGGCCAAACAAACAGCGGAAACGCCCTTA 1200
DB 1173 GGCATCTCTCCACAAAAGAGAAAACGTCAGGCCAAACAAACAGCGGAAACGCCCTTA 1232
QY 1201 AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACT 1260
DB 1233 AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACT 1292
QY 1261 GGATTTGGCTCCCGCGGGGTATACGCTTTTACTGCGACGAGAAATGCCCTTTTCTC 1320
DB 1293 GGATTTGGCTCCCGCGGGGTATACGCTTTTACTGCGACGAGAAATGCCCTTTTCTC 1352
QY 1321 TGGCTGATCATCTGAACCTCCACTAATCATGATCCATTTGTTGACAGCTTGTCTGTTA 1380
DB 1353 TGGCTGATCATCTGAACCTCCACTAATCATGATCCATTTGTTGACAGCTTGTCTGTTA 1412
QY 1381 ACTCTAAGATTCTTAAGGCATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
DB 1413 ACTCTAAGATTCTTAAGGCATGCTGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGT 1472
QY 1441 ACCTTGACGAGAAAGGTTGTTAATTAAGAACTATCAGGACATGTTGTTGGAGGGTT 1500
DB 1473 ACCTTGACGAGAAAGGTTGTTAATTAAGAACTATCAGGACATGTTGTTGGAGGGTT 1532
QY 1501 GTGGGTGCTGTAGTACAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1547
DB 1533 GTGGGTGCTGTAGTACAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1579

RESULT 3
US-08-925-779-3
; Sequence 3, Application US/08925779
; Patent No. 6245889
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: No. 6245889el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.


```
STREET: 87 CAMBRIDGE PARK DRIVE
CITY: CAMBRIDGE
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,779
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,847
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: 5160C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
CELL TYPE: Osteosarcoma Cell Line
CELL LINE: U-2OS
IMMEDIATE SOURCE:
LIBRARY: U2OS cDNA in Lambda GT10
CLONE: Lambda U2OS-39
POSITION IN GENOME:
UNITS: bp
FEATURE:
NAME/KEY: CDS
LOCATION: 356..1546
FEATURE:
NAME/KEY: .mat_peptide
LOCATION: 1202..1543
FEATURE:
NAME/KEY: mRNA
LOCATION: 14..1607
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NAME/KEY: sig_peptide
LOCATION: 356..424
US-08-925-779-3

Query Match 100.0%; Score 1547; DB 3; Length 1607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTCTTGAACCTTCAGGGAGATTAACCTTCGGCAGCCCACTTTTGGCGCGGTGCTT 60
Db 33 GGGGACTCTTGAACCTTCAGGGAGATTAACCTTCGGCAGCCCACTTTTGGCGCGGTGCTT 92
Qy 61 TGCCCCGAGCGAGCTGCTTCGCCATCTCCAGAGCCCAACCGCCCTCCACTCTCTCGGCCT 120
Db 93 TGCCCCGAGCGAGCTGCTTCGCCATCTCCAGAGCCCAACCGCCCTCCACTCTCTCGGCCT 152
Qy 121 TGCCCGACACTGAGACGCTGTTCACGCTGAAAGAGAGACTGCGCGGCGCGCACCCGG 180
Db 153 TGCCCGACACTGAGACGCTGTTCACGCTGAAAGAGAGACTGCGCGGCGCGCACCCGG 212
Qy 181 GAGAGGAGGAGGCAAGAAAGGACCGGACATTCGGTCTCTTGGCCAGGTCCTTTTGACC 240
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Db 213 GAGAGGAGGAGGCAAGAAAGGAAACGGACATTCGGTCTCTTGGCCAGGTCCTTTTGACC 272
Qy 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGGACGCTGTCCCGCGTCTTCTTAGACGGA 300
Db 273 AGAGTTTTTCCATGTGACGCTCTTTCAATGGACGCTGTCCCGCGTCTTCTTAGACGGA 332
Qy 301 CTGCGGTCTCTTAAAGGTGCAACATGTGTGCGCGGACCCCGTGTCTTCTTAGCGTTGCTGC 360
Db 333 CTGCGGTCTCTTAAAGGTGCAACATGTGTGCGCGGACCCCGTGTCTTCTTAGCGTTGCTGC 392
Qy 361 TTCCCCAGAGTCTCTTGGGCGGCGCGCTCGTTCCGGAGCTGGCGCGCAGGAAGT 420
Db 393 TTCCCCAGAGTCTCTTGGGCGGCGCGCTCGTTCCGGAGCTGGCGCGCAGGAAGT 452
Qy 421 TCGCGCGGCGGTCTGTGGGCGCGCGCTCATCCAGCCCTCTGACGAGTCTGAGCGAGT 480
Db 453 TCGCGCGGCGGTCTGTGGGCGCGCGCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGT 512
Qy 481 TCGAGTTTGGCGGTCTGTGAGCATGTTCGGCTCTGAAACAGAGACCCACCCAGCAGGGACG 540
Db 513 TCGAGTTTGGCGGTCTGTGAGCATGTTCGGCTCTGAAACAGAGACCCACCCAGCAGGGACG 572
Qy 541 CCGTGTGCCCGCTCATATGCTAGACCTGTATCGCAGGCACTCAGGTCAGCGGCTCAC 600
Db 573 CCGTGTGCCCGCTCATATGCTAGACCTGTATCGCAGGCACTCAGGTCAGCGGCTCAC 632
Qy 601 CCGCCCCAGACCCCGTGTGGAGGGCAGCAGCCGAGCCAACTGTGTGCGCAGCTTCC 660
Db 633 CCGCCCCAGACCCCGTGTGGAGGGCAGCAGCCGAGCCAACTGTGTGCGCAGCTTCC 692
Qy 661 ACCATGAAGAAATCTTTGGAAGAACTACAGAAACGAGTGGGAAACAAACCCGGAGATTCT 720
Db 693 ACCATGAAGAAATCTTTGGAAGAACTACAGAAACGAGTGGGAAACAAACCCGGAGATTCT 752
Qy 721 TCTTTAATTTAAGTTCTATCCCGCAGGAGGTTTATCAGCTCAGCAGAGCTTCAGGTTT 780
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Qy 841 TTTATGAAATCATAAACCTTGCAACAGCCAACTTCGAAATTCCTCCGTCGACAGACTTTGG 900
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Qy 901 ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 960
Db 933 ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG 992
Qy 961 TGATGCGGTGGAAGTGCACAGGGACACGCCAACTAGGATTCGTTGGTGGAAAGTGCCCACT 1020
Db 993 TGATGCGGTGGAAGTGCACAGGGACACGCCAACTAGGATTCGTTGGTGGAAAGTGCCCACT 1052
Qy 1021 TGGAGGAGAAACAAAGGTGTCTCCAGAGACATGTTAGGATTAAGCAGGTCTTTGACCCAG 1080
Db 1053 TGGAGGAGAAACAAAGGTGTCTCCAGAGACATGTTAGGATTAAGCAGGTCTTTGACCCAG 1112
Qy 1081 ATGAACACAGCTGTCACAGATAAGGCCATTTGTAGTAACTTTTGGCCATGATCGAAAG 1140
Db 1113 ATGAACACAGCTGTCACAGATAAGGCCATTTGTAGTAACTTTTGGCCATGATCGAAAG 1172
Qy 1141 GGCATCTCTCCACAAAGAGAGAAACAGTCAAGCAACAAACAAACAGCGGAAACGCCCTTA 1200
Db 1173 GGCATCTCTCCACAAAGAGAGAAACAGTCAAGCAACAAACAAACAGCGGAAACGCCCTTA 1232
Qy 1201 AGTCCAGCTGTAGAGACACCTTTTGTAGTGGACTTCAGTGAGCTGGGTGGAAATGACT 1260
Db 1233 AGTCCAGCTGTAGAGACACCTTTTGTAGTGGACTTCAGTGAGCTGGGTGGAAATGACT 1292
Qy 1261 GGATTGTGGTCCCGCGGGGTATCACGCTTTTACTGCCAGGAGAAATGCCCTTTTCTC 1320
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Db 1293 GGATTGTGGCTCCCGGGGTATACGGCTTTTACTGCGCACGGAGAAATGCCCCCTTTTCCTC 1352
Qy 1321 TGGCTGATCATCTGAACCTCACTAATCATGCTTTCAGACGTTGGTCAACTCTGTTA 1380
Db 1353 TGGCTGATCATCTGAACCTCACTAATCATGCTTTCAGACGTTGGTCAACTCTGTTA 1412
Qy 1381 ACTCTAAGATTCCTTAAGGCATCTGTGTCGCCGACGAACTCAGTGTCTATCTCGATGCTGT 1440
Db 1413 ACTCTAAGATTCCTTAAGGCATCTGTGTCGCCGACGAACTCAGTGTCTATCTCGATGCTGT 1472
Qy 1441 ACTCTGACGAGAAATGAAGGTTGTATTAAGAACTATCAGACGATGGTTGTGGAGGTT 1500
Db 1473 ACTCTGACGAGAAATGAAGGTTGTATTAAGAACTATCAGACGATGGTTGTGGAGGTT 1532
Qy 1501 GTGGGTGCTGTAGTACAGCAAAATTAATACATAAATATATATA 1547
Db 1533 GTGGGTGCTGTAGTACAGCAAAATTAATACATAAATATATATA 1579

RESULT 4
5166058-3
; Patent No. 5166058
; APPLICANT: WANG, ELIZABETH A.; WOZNEY, JOHN M.; RPSN, VICKI A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING THE OSTEOINDUCTIVE
; PROTEINS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/378,537
; FILING DATE: 11-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 179,100
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: 28,285
; FILING DATE: 20-MAR-1987
; APPLICATION NUMBER: 943,332
; FILING DATE: 17-DEC-1986
; APPLICATION NUMBER: 880,776
; FILING DATE: 01-JUL-1986
; SEQ ID NO:3
; LENGTH: 1607
5166058-3

Query Match 100.0%; Score 1547; DB 9; Length 1607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTTCTTGAACCTTGACGGAGAAATACTTGGCGACCCCACTTTGGCGCGGTGCCTT 60
Db 33 GGGGACTTCTTGAACCTTGACGGAGAAATACTTGGCGACCCCACTTTGGCGCGGTGCCTT 92

Qy 61 TGGCCGAGGAGCTGCTTCCGATCTCCGAGCCCAACCGCCCTTCACTCTCGGCT 120
Db 93 TGGCCGAGGAGCTGCTTCCGATCTCCGAGCCCAACCGCCCTTCACTCTCGGCT 152

Qy 121 TGGCCGACACTGAGACGCTGTTCCAGCTGAAAGAGAGACTGCGCGCGGACCCGG 180
Db 153 TGGCCGACACTGAGACGCTGTTCCAGCTGAAAGAGAGACTGCGCGCGGACCCGG 212

Qy 181 GAGAGGAGGAGGCAAGAAAGGAAACGACATTCGGTCTTTGGCCGACGCTTTTGACC 240
Db 213 GAGAGGAGGAGGCAAGAAAGGAAACGACATTCGGTCTTTGGCCGACGCTTTTGACC 272

Qy 241 AGAGTTTTCATGTGGAGCTCTTTCAATGACGTGTCCCGGCTTCTTACACGGA 300
Db 273 AGAGTTTTCATGTGGAGCTCTTTCAATGACGTGTCCCGGCTTCTTACACGGA 332

Qy 301 CTGCGGTCTCTTAAAGTTCGACATGTGGCGGGACCGCTGCTTCTAGGTTGCTGC 360
Db 333 CTGCGGTCTCTTAAAGTTCGACATGTGGCGGGACCGCTGCTTCTAGGTTGCTGC 392

Qy 361 TTTCCCGAGTCTCTTGGCGGCGGCTGCTGCTTCCGAGCTGGGCGCGCAGGAAAT 420
Db 393 TTTCCCGAGTCTCTTGGCGGCGGCTGCTGCTTCCGAGCTGGGCGCGCAGGAAAT 452

Qy 421 TCGCGGCGGCTGCTGCGGCGCGCCCTCATCCAGCCCTCTGACGAGGTCTTGAGCGAGT 480
Db 453 TCGCGGCGGCTGCTGCGGCGCGCCCTCATCCAGCCCTCTGACGAGGTCTTGAGCGAGT 512

Qy 481 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTTGAACACAGAGACCCACCCCGAGCGGAG 540
Db 513 TCGAGTTGCGGCTGCTCAGCATGTTTCGGCTTGAACACAGAGACCCACCCCGAGCGGAG 572

Qy 541 CGGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGGCTCAC 600
Db 573 CGGTGGTCCCGCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGGGCTCAC 632

Qy 601 CGCGCCACAGACACCGGTTGAGAGGGCAGCCAGCGGAGCCCACTGTGCGCAGCTTCC 660
Db 633 CGCGCCACAGACACCGGTTGAGAGGGCAGCCAGCGGAGCCCACTGTGCGCAGCTTCC 692

Qy 661 ACCATGAAGAATCTTTTGAAGAATCTACAGAAACGAGTGGGAAACAAACCCGAGATTC 720
Db 693 ACCATGAAGAATCTTTTGAAGAATCTACAGAAACGAGTGGGAAACAAACCCGAGATTC 752

Qy 721 TCTTTAATTTAAGTCTATCCCGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db 753 TCTTTAATTTAAGTCTATCCCGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 812

Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAACAATAGCAGTTTCCATCACCGAAATTAATA 840
Db 813 TCCGAGAACAGATGCAAGATGCTTTAGGAACAATAGCAGTTTCCATCACCGAAATTAATA 872

Qy 841 TTTATGAATCATATAAACTCTGCAACAGCCAACTCGAAATTCCTCGTACCCAGACTTTGG 900
Db 873 TTTATGAATCATATAAACTCTGCAACAGCCAACTCGAAATTCCTCGTACCCAGACTTTGG 932

Qy 901 ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTACCCCGCTG 960
Db 933 ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTACCCCGCTG 992

Qy 961 TGATGCGGTGACTGTCACAGGACACGCAACCATGGAATTCGTGTGGAAGTGGCCACT 1020
Db 993 TGATGCGGTGACTGTCACAGGACACGCAACCATGGAATTCGTGTGGAAGTGGCCACT 1052

Qy 1021 TGGAGGAGAAACAAAGGTGCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGCAACCAAG 1080
Db 1053 TGGAGGAGAAACAAAGGTGCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGCAACCAAG 1112

Qy 1081 ATGAACACAGCTGCTCAGATTAAGCCATTCCTAGTAACTTTTGGCCATGATGGAAG 1140
Db 1113 ATGAACACAGCTGCTCAGATTAAGCCATTCCTAGTAACTTTTGGCCATGATGGAAG 1172

Qy 1141 GGCATCTCTCCAAAAAGAGAAACGTCAGCCCAACACAAAAACAGCGGAAACGCCCTTA 1200
Db 1173 GGCATCTCTCCAAAAAGAGAAACGTCAGCCCAACACAAAAACAGCGGAAACGCCCTTA 1232

Qy 1201 AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGAATTCAGTGACCGTGGGTGGAATGACT 1260
Db 1233 AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGAATTCAGTGACCGTGGGTGGAATGACT 1292

Qy 1261 GGAATGTGGCTCCCGCGGGGTATACGCGCTTTTACTGCCACGGAATGCCCCTTTTCTC 1320
Db 1293 GGAATGTGGCTCCCGCGGGGTATACGCGCTTTTACTGCCACGGAATGCCCCTTTTCTC 1352

Qy 1321 TGGCTGATCATCTGAACCTCACTAATCATGCTTGTTCAGACGTTGGTCAACTCTGTTA 1380
Db 1353 TGGCTGATCATCTGAACCTCACTAATCATGCTTGTTCAGACGTTGGTCAACTCTGTTA 1412

Qy 1381 ACTCTAAGATTCCTTAAGGCATGCTGTGTCGCCGACGAACTCAGTGTCTATCTCGATGCTGT 1440
Db 1413 ACTCTAAGATTCCTTAAGGCATGCTGTGTCGCCGACGAACTCAGTGTCTATCTCGATGCTGT 1472

Qy 1441 ACCTTGAACGAGATGAAGGTTGTATTAAGAACTATCAGACGATGGTTGTGGAGGTT 1500
Db 1473 ACCTTGAACGAGATGAAGGTTGTATTAAGAACTATCAGACGATGGTTGTGGAGGTT 1532

RESULT 7

US-08-469-411-1
; Sequence 1, Application US/08469411
; Patent No. 6190880
; GENERAL INFORMATION:
; APPLICANT: Israel, David
; Wolfman, Neil M.
; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
; Heterodimers, Compositions and Methods of Use.
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,411
; FILING DATE: 06-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI-5192B-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8622
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1543
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-469-411-1

Query Match 99.9%; Score 1545.4; DB 3; Length 1607;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GGGACTTCTTGAACCTTCAGGGAGATAA	CTTGGCGACCCCACTTTTGGCGCGGTGCTT	60
Db	33	GGGGACTTCTTGAACCTTCAGGGAGATAA	CTTGGCGACCCCACTTTTGGCGCGGTGCTT	92
Qy	61	TGCCCCAGCGAGCTGCTCCGCACTCCGAG	CCCAACCCGCTCCCACTCTCCGCT	120
Db	93	TGCCCCAGCGAGCTGCTCCGCACTCCGAG	CCCAACCCGCTCCCACTCTCCGCT	152
Qy	121	TGCCCGACACTGAGACGCTGTTCCAGCGT	TCCGAGAGAGACTCGCGCGCGCACCGG	180
Db	153	TGCCCGACACTGAGACGCTGTTCCAGCGT	TCCGAGAGAGACTCGCGCGCGCACCGG	212
Qy	181	GAGAGGAGGAGGAGGAGGAGGAGGAGGAG	GAGGAGGAGGAGGAGGAGGAGGAGGAGG	240
Db	213	GAGAGGAGGAGGAGGAGGAGGAGGAGGAG	GAGGAGGAGGAGGAGGAGGAGGAGGAGG	272
Qy	241	AGAGTTTTCATGTGAGCGCTCTTTCAATG	GAGCTGTCCCGCGTCTCTTAGACGGA	300
Db	273	AGAGTTTTCATGTGAGCGCTCTTTCAATG	GAGCTGTCCCGCGTCTCTTAGACGGA	332
Qy	301	CTCGGGTCTCTAAAGTTCAGACCATGTGT	GGCGGAGACCGCTGTCTTCTAGCGTGTGC	360
Db	333	CTCGGGTCTCTAAAGTTCAGACCATGTGT	GGCGGAGACCGCTGTCTTCTAGCGTGTGC	392

Qy	361	TTCCCCAGAGTCTCTCGGGCGCGCGCTG	CGCTCGCTTCGGAGCTGCGCGCAGGAAGT	420
Db	393	TTCCCCAGAGTCTCTCGGGCGCGCGCTG	CGCTTCGGAGCTGCGCGCAGGAAGT	452
Qy	421	TCGGCGGGCGGTGCTCGGGCGCGCCCTC	ATCCAGCCCTCTGACGAGTCTCTGAGCGAGT	480
Db	453	TCGGCGGGCGGTGCTCGGGCGCGCCCTC	ATCCAGCCCTCTGACGAGTCTCTGAGCGAGT	512
Qy	481	TCGAGTTGCGGCTGCTCAGCATGTTTGG	CGCTGAAACAGAGACCCACCCGAGCGGACG	540
Db	513	TCGAGTTGCGGCTGCTCAGCATGTTTGG	CGCTGAAACAGAGACCCACCCGAGCGGACG	572
Qy	541	CGGTGTTGCCCTTACATGCTAGACCTGT	ATCGCAGGCACTCAGTTCAGCGGCTCAC	600
Db	573	CGGTGTTGCCCTTACATGCTAGACCTGT	ATCGCAGGCACTCAGTTCAGCGGCTCAC	632
Qy	601	CCGCCCCAGACCAACCGGTTGGAGAGG	CGCAGCCAGGCAACATCTGTGCGCAGCTTCC	660
Db	633	CCGCCCCAGACCAACCGGTTGGAGAGG	CGCAGCCAGGCAACATCTGTGCGCAGCTTCC	692
Qy	661	ACCATGAAGAATCTTTGGAAAGAACTAC	CAGAAACGAGTGGGAAACAAACCCGAGATCT	720
Db	693	ACCATGAAGAATCTTTGGAAAGAACTAC	CAGAAACGAGTGGGAAACAAACCCGAGATCT	752
Qy	721	TCTTTAATTTAAGTTCTATCCCGCAGG	AGGTTTATCAGCTCAGAGAGCTTCAGGTTT	780
Db	753	TCTTTAATTTAAGTTCTATCCCGCAGG	AGGTTTATCAGCTCAGAGAGCTTCAGGTTT	812
Qy	781	TCCGAGAACAGATGCAAGATGCTTTTAG	AGAAACAATAGCAGTTCATCCAGCAATTAATA	840
Db	813	TCCGAGAACAGATGCAAGATGCTTTTAG	AGAAACAATAGCAGTTCATCCAGCAATTAATA	872
Qy	841	TTTATGAATCATAAACCTTGCAACAGC	CAACTCGAAATTCCTCGTGACCACTTTTGG	900
Db	873	TTTATGAATCATAAACCTTGCAACAGC	CAACTCGAAATTCCTCGTGACCACTTTTGG	932
Qy	901	ACACAGGTTGGTGAATCAGAAATGCA	AGAGTGGGAAAGTTTGTGATCAACCCCGCTG	960
Db	933	ACACAGGTTGGTGAATCAGAAATGCA	AGAGTGGGAAAGTTTGTGATCAACCCCGCTG	992
Qy	961	TGATGCGGTGGAATGCAAGGACACG	CCCAACCATGATTCGTGGTGGAAAGTGC	1020
Db	993	TGATGCGGTGGAATGCAAGGACACG	CCCAACCATGATTCGTGGTGGAAAGTGC	1052
Qy	1021	TGAGAGGAGAAACAGGTGCTCCAGAG	ACATGTTAGGATAAGCAGTCTTTTGACCAAG	1080
Db	1053	TGAGAGGAGAAACAGGTGCTCCAGAG	ACATGTTAGGATAAGCAGTCTTTTGACCAAG	1112
Qy	1081	ATGAACACAGCTGTCACAGTAAAGG	CCATTCGTAGTAATTTTGGCCATGATG	1140
Db	1113	ATGAACACAGCTGTCACAGTAAAGG	CCATTCGTAGTAATTTTGGCCATGATG	1172
Qy	1141	GGCATCTCTCCACAAAGAGAAAAAC	GTCAAGCCAAACAAACACACGCGAAAC	1200
Db	1173	GGCATCTCTCCACAAAGAGAAAAAC	GTCAAGCCAAACAAACACACGCGAAAC	1232
Qy	1201	AGTCACAGCTGTAAGAGACACCTTTT	GTACGTGAGCTTCAGTACGTGGGTGGAATG	1260
Db	1233	AGTCACAGCTGTAAGAGACACCTTTT	GTACGTGAGCTTCAGTACGTGGGTGGAATG	1292
Qy	1261	GGATTGTGGCTCCCGCGGGGTATC	ACGCCCTTTTACTGCCACGGAATGCCCTT	1320
Db	1293	GGATTGTGGCTCCCGCGGGGTATC	ACGCCCTTTTACTGCCACGGAATGCCCTT	1352
Qy	1321	TGGCTGATCATCTGAACTCCAAT	CATGCAATGTTTTCAGACGTTGGTCACTGT	1380
Db	1353	TGGCTGATCATCTGAACTCCAAT	CATGCAATGTTTTCAGACGTTGGTCACTGT	1412
Qy	1381	ACTCTAAGATTCCTAAGGCACTGTGT	TCGCGACAGAACTCAGTGTCTATCTCGATG	1440
Db	1413	ACTCTAAGATTCCTAAGGCACTGTGT	TCGCGACAGAACTCAGTGTCTATCTCGATG	1472

QY 1441 ACCTTGACGAGAAATGAAAGGTTGTTATTAAAGAACTATCAGGACATGTTGTGGAGGTT 1500
Db 1473 ACCTTGACGAGAAATGAAAGGTTGTTATTAAAGAACTATCAGGACATGTTGTGGAGGTT 1532
QY 1501 GTGGGTGTCGTAGTACAGCAAAATTAATACATAAATATATATATA 1547
Db 1533 GTGGGTGTCGTAGTACAGCAAAATTAATACATAAATATATATATA 1579

RESULT 8
US-09-780-601A-1
; Sequence 1, Application US/09780601A
; Patent No. 6593109
; GENERAL INFORMATION:
; APPLICANT: Israel, David
; APPLICANT: Wolfman, Neil M.
; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
; TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/780,601A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,411
; FILING DATE: 06-Jun-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI-5192B-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8622
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1543
US-09-780-601A-1

Query Match 99.9%; Score 1545.4; DB 3; Length 1607;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGACTTCTTCAACTTTCAGGAGAAATTAATTCGGCACCCCACTTTGGCCGGTGCCCTT 60
Db 33 GGGGACTTCTTCAACTTTCAGGAGAAATTAATTCGGCACCCCACTTTGGCCGGTGCCCTT 92
QY 61 TGCCCCCAGCGAGCCTCTTCGCCCATCTCCGAGCCCCCACCGCCCTCCCACTCTCCGGCCT 120
Db 93 TGCCCCCAGCGAGCCTCTTCGCCCATCTCCGAGCCCCCACCGCCCTCCCACTCTCCGGCCT 152
QY 121 TGCCCCGACACTGAGACGCTGTTCCCGACCGTGAAGAGAGACTGCGCGCGCGGCGACCCGG 180
Db 153 TGCCCCGACACTGAGACGCTGTTCCCGACCGTGAAGAGAGACTGCGCGCGCGGCGACCCGG 212

QY 181 GAGAAGGAGGAGGCAAAAGAAAGGAAACGGAACATTCGGTCTTGGCCAGGTCCTTTGACC 240
Db 213 GAGAAGGAGGAGGCAAAAGAAAGGAAACGGAACATTCGGTCTTGGCCAGGTCCTTTGACC 272
QY 241 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGGAAGTGTCCCGCGTGTCTTTCTTAGACGGA 300
Db 273 AGAGTTTTTCCATGTGAGCGCTCTTTCAATGGAAGTGTCCCGCGTGTCTTTCTTAGACGGA 332
QY 301 CTGCGGTCTCTTAAAGGTCGACCATGTGGCGCGGACCCGCTGTCTTCTAGGTTGTGTC 360
Db 333 CTGCGGTCTCTTAAAGGTCGACCATGTGGCGCGGACCCGCTGTCTTCTAGGTTGTGTC 392
QY 361 TTCCCCAGGTCTCTCTGCGCGCGCGGTGCGCTCTGTTCCGAGAGTGTGGCGCGCAGGAAGT 420
Db 393 TTCCCCAGGTCTCTCTGCGCGCGCGGTGCGCTCTGTTCCGAGAGTGTGGCGCGCAGGAAGT 452
QY 421 TCGCGCGCGGTCTGTCGCGCGCGCGCTCATCCGAGCCCTCTGACGAGTCTCTGACGAGT 480
Db 453 TCGCGCGCGGTCTGTCGCGCGCGCGCTCATCCGAGCCCTCTGACGAGTCTCTGACGAGT 512
QY 481 TCGAGTTGCGGCTCTCAGCATGTTTGGGCTTGAACAGAGACCCACCCAGCAGGAGCG 540
Db 513 TCGAGTTGCGGCTCTCAGCATGTTTGGGCTTGAACAGAGACCCACCCAGCAGGAGCG 572
QY 541 CCGTGTGCCCCCTTACATGTAGACCTGTATCGCAGGCATCTCAGTCTCAGCGCGGCTCAC 600
Db 573 CCGTGTGCCCCCTTACATGTAGACCTGTATCGCAGGCATCTCAGTCTCAGCGCGGCTCAC 632
QY 601 CCGCCCCAGACACCGGTTGAGAGGCGCAGCCAGCGAGCCAACTCTGTGGCAGCTTCC 660
Db 633 CCGCCCCAGACACCGGTTGAGAGGCGCAGCCAGCGAGCCAACTCTGTGGCAGCTTCC 692
QY 661 ACCATGAGAAATCTTTGGAAGAACTACCCAGAAACGAGTGGGAAACAAACCCGAGATCT 720
Db 693 ACCATGAGAAATCTTTGGAAGAACTACCCAGAAACGAGTGGGAAACAAACCCGAGATCT 752
QY 721 TCTTTAATTTAAGTTCTATCCCGCAGGAGGAGTTTATCACCTCAGCAGAGCTTCAAGTTT 780
Db 753 TCTTTAATTTAAGTTCTATCCCGCAGGAGGAGTTTATCACCTCAGCAGAGCTTCAAGTTT 812
QY 781 TCCGAGAAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCAGCGAATTAATA 840
Db 813 TCCGAGAAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCAGCGAATTAATA 872
QY 841 TTTATGAATCATAAACCTGCAACAGCCAACTCGAATTCCTCGTACGACGACTTTGG 900
Db 873 TTTATGAATCATAAACCTGCAACAGCCAACTCGAATTCCTCGTACGACGACTTTGG 932
QY 901 ACACGAGTTGGTGAATCAGAAATGCAAGCAGTGGGAAAGTTTGTATGTCAACCCCGCTG 960
Db 933 ACACGAGTTGGTGAATCAGAAATGCAAGCAGTGGGAAAGTTTGTATGTCAACCCCGCTG 992
QY 961 TGATGCGGTGACTGCAAGGAGACGCAACCAATGGATTCGTGTGGAAGTGGCCACT 1020
Db 993 TGATGCGGTGACTGCAAGGAGACGCAACCAATGGATTCGTGTGGAAGTGGCCACT 1052
QY 1021 TGGAGGAGAAACAAAGGTCTCTCAAGAGACATGTTAGGTAAGCAGTCTTTGCAACCAAG 1080
Db 1053 TGGAGGAGAAACAAAGGTCTCTCAAGAGACATGTTAGGTAAGCAGTCTTTGCAACCAAG 1112
QY 1081 ATGAACACAGCTGGTCAAGATTAAGCCATTTGCTAGTAACCTTTTGGCCATGATGGAAG 1140
Db 1113 ATGAACACAGCTGGTCAAGATTAAGCCATTTGCTAGTAACCTTTTGGCCATGATGGAAG 1172
QY 1141 GGCATCTCTCCAAAAAGAGAAAAACGTCAGCCAAAACAAAAACAGCGGAAACGCCCTTA 1200
Db 1173 GGCATCTCTCCAAAAAGAGAAAAACGTCAGCCAAAACAAAAACAGCGGAAACGCCCTTA 1232
QY 1201 AGTCAGCTGTAAAGAGACACCTTTGTAGTGGACTTCACTGACGCTGGGTGGGAATGACT 1260
Db 1233 AGTCAGCTGTAAAGAGACACCTTTGTAGTGGACTTCACTGACGCTGGGTGGGAATGACT 1292
QY 1261 GGATTTGGCTCCCCCGGGGTATCACGCTTTTACTGCGCAGGAGAAATGCCCCCTTTTCCTC 1320

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Db 1293 GGAATGGCTCCCGGGGATACGGCTTTTACTGCCAGGAGATGCCCTTTCTC 1352
Qy 1321 TGGCTGATCATCTGAACTCCACTAATCATGCAATGTTGTCAGACGTTGGTCAACTCTGTTA 1380
Db 1353 TGGCTGATCATCTGAACTCCACTAATCATGCAATGTTGTCAGACGTTGGTCAACTCTGTTA 1412
Qy 1381 ACTCTAGATTCCTAAGGCACTGCTGTGTCGCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
Db 1413 ACTCTAGATTCCTAAGGCACTGCTGTGTCGCCGACAGAACTCAGTGCTATCTCGATGCTGT 1472
Qy 1441 ACCTTGACGAGATGAAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Db 1473 ACCTTGACGAGATGAAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGAGGGTT 1532
Qy 1501 GTGGGTGTCGTAGTACAGCAAAATTAATAATATATATATATA 1547
Db 1533 GTGGGTGTCGTAGTACAGCAAAATTAATAATATATATATA 1579

RESULT 9
US-09-949-016-4668
; Sequence 4668, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C6001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4668
; LENGTH: 2185
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4668
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Query Match 99.9%; Score 1545.4; DB 3; Length 2185;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGACTTCTTGAACCTTCAGGAGATAAATCTGGCACCCCACTTTTGGCGCGGTGCTT 60
Db 45 GGGGACTTCTTGAACCTTCAGGAGATAAATCTGGCACCCCACTTTTGGCGCGGTGCTT 104
Qy 61 TGCCCCAGCGAGCTGCTTCCCATCTCCAGACCCCACTCCCTCCCTCGGCT 120
Db 105 TGCCCCAGCGAGCTGCTTCCCATCTCCAGACCCCACTCCCTCCCTCGGCT 164
Qy 121 TGCCCCAGCACTGAGACGCTGTTCCAGCGTGAAGAGAGACTCGCGGCGCGCACCCGG 180
Db 165 TGCCCCAGCACTGAGACGCTGTTCCAGCGTGAAGAGAGACTCGCGGCGCGCACCCGG 224
Qy 181 GAGAAGGAGGAGGCAAGAAAGGACGACATTTGGTCCCTTGGCCAGGTCCTTTGACC 240
Db 225 GAGAAGGAGGAGGCAAGAAAGGACGACATTTGGTCCCTTGGCCAGGTCCTTTGACC 284
Qy 241 AGAGTTTTTCAATGTGACGCTCTTTCAATGACGCTGTCCCGCGGTCTCTTAGACGGA 300
Db 285 AGAGTTTTTCAATGTGACGCTCTTTCAATGACGCTGTCCCGCGGTCTCTTAGACGGA 344
Qy 301 CTGCGGCTCTCTAAGGTCGACCAATGTTGGCGCGGACCCGCTGCTTCTAGCTGTGTC 360
Db 345 CTGCGGCTCTCTAAGGTCGACCAATGTTGGCGCGGACCCGCTGCTTCTAGCTGTGTC 404
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Qy 361 TTCCCCAGGTCCTCTCGGCGCGCGGCTGGCTCGTTCCGAGCTGCGCGCGCAGGAGT 420
Db 405 TTCCCCAGGTCCTCTCGGCGCGCGGCTGGCTCGTTCCGAGCTGCGCGCGCAGGAGT 464
Qy 421 TCGCGGCGGCGTGTGTGCGGCGCGGCTCATCCAGCCCTCTGACGAGGTCCTGAGCGAGT 480
Db 465 TCGCGGCGGCGTGTGTGCGGCGCGGCTCATCCAGCCCTCTGACGAGGTCCTGAGCGAGT 524
Qy 481 TCGAGTTGCGGCTGTGTGAGCATGTTTGGGCTTGAAAACAGAGACCCACCCGAGGAGACG 540
Db 525 TCGAGTTGCGGCTGTGTGAGCATGTTTGGGCTTGAAAACAGAGACCCACCCGAGGAGACG 584
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Qy 721 TCTTTAATTTAAGTTCTATCCCAAGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db 765 TCTTTAATTTAAGTTCTATCCCAAGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 824
Qy 781 TCCGAGAACAGATGCAAGATGCTTTTAGGAAACAATAGCAGTTTCCATCACCAGATTATA 840
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Db 885 TTTATGAATAATCAAAAACCTTGCAACAGCCAACTCGAAAATTCGCCGTGACAGACTTTGG 944
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RESULT 10

US-07-679-451-1
; Sequence 1, Application US/07679451
; Patent No. 531898
; GENERAL INFORMATION:
; APPLICANT: Israel, David I.
; TITLE OF INVENTION: IMPROVED PRODUCTION OF RECOMBINANT
; TITLE OF INVENTION: BONE-INDUCING PROTEINS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,451
; FILING DATE: 19910402
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/179,100
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: GI 5180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; IMMEDIATE SOURCE:
; CLONE: HUMBP11-CDNA-39
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..355
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1544..1607
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 5,013,649
; FILING DATE: 08-APR-1988
; PUBLICATION DATE: 07-MAY-1991

US-07-679-451-1

Query Match 99.8%; Score 1543.8; DB 2; Length 1607;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1545; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 721 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCACCTCAGCAGAGCTTCAAGTTT 780
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QY 1141 GGCATCTCTCCACAAAAGAGAAAACGCTCAAGCCAAAACACAAACAGCGGAAACGCCTTTA 1200
Db 1173 GGCATCTCTCCACAAAAGAGAAAACGCTCAAGCCAAAACACAAACAGCGGAAACGCCTTTA 1232
QY 1201 AGTCAGCTGTAAAGACACACCCCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACT 1260
Db 1233 AGTCAGCTGTAAAGACACACCCCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACT 1292
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RESULT 11

US-07-841-646-4

; Sequence 4, Application US/07841646

; Patent No. 5266683

; GENERAL INFORMATION:

; APPLICANT: OPPERMANN, HERMANN

; APPLICANT: OZKAYNAK, ENGIN

; APPLICANT: KUBERASAMPATH, THANGAVEL

; APPLICANT: RUEGER, DAVID C.

; APPLICANT: PANG, ROY H.L.

; TITLE OF INVENTION: OSTEOGENIC DEVICES

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

; STREET: 53 STATE STREET

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: U.S.A.

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/841,646

; FILING DATE: 19920221

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 810,560

; FILING DATE: 20-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 827,052

; FILING DATE: 28-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 660,162

; FILING DATE: 22-FEB-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 621,988

; FILING DATE: 04-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 621,849

; FILING DATE: 04-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 621,849

; FILING DATE: 04-DEC-1990

; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..1196
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "CBMP2A"
; OTHER INFORMATION: /note= "CBMP2A (CDNA)"
; US-07-841-646-4
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 496 TCAGCATGTTGGGCTTGAAACAGAGAGCCACCCCGCAGGAGCGCGCTGCTGTCGCCCT 555
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Db 301 GGTGGAGAGGCGCAGCAGCAGCAGCAACATGTGCGCAGTTCACCATGAAGATCTT 360
Qy 676 TGGAGAACTACCAAGAAAGAGTGGGAAACCAACCCGAGATCTCTTTAAATTAAGTT 735
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RESULT 12

US-07-901-703-14

; Sequence 14, Application US/07901703
; Patent No. 5344654
; GENERAL INFORMATION:
; APPLICANT: RUEGER, DAVID C
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZAKAYNAK, ERGIN
; TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
; TITLE OF INVENTION: OSTEOGENIC PROPERTIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/901,703
; FILING DATE: 19920616
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: CDS /function= "OSTEOGENIC PROTEIN"
; LOCATION: 9..1196
; OTHER INFORMATION: /product= "BMP2A"
; OTHER INFORMATION: /note= "BMP2A (CDNA) "
; US-07-901-703-14

Query Match 79.3%; Score 1227.2; DB 2; Length 1260;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 316 GGTGCACCATGTTGGTCGGGACCCGCTGCTTTCTAGCGTTGCTTCCAGGTCCTCC 375
Db 1 GGTGCACCATGTTGGTCGGGACCCGCTGCTTTCTAGCGTTGCTTCCAGGTCCTCC 60
Qy 376 TGGCGGCGCGGCTGGCTTCGTTCCGAGCTTGGGCGCGCAGGAAGTTTCGCGCGGCGTCT 435
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Db 181 TCAGCATGTTGGGCTGAAACAGAGACCCACCCAGCAGGAGACCGCGTGTGCCCCCT 240
Qy 556 ACATGCTAGACTGTATCGCAGGCACTCAGGTACGCGGGCTCACCCGCCCCAGACACACC 615

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RESULT 13
US-08-147-023-4
; Sequence 4, Application US/08147023
; Patent No. 546845
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN

APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HORWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/147,023
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000

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TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
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; NAME/KEY: CDS
; LOCATION: 9..1196
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "CBMP2A"
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US-08-147-023-4

Query Match 79.3%; Score 1227.2; DB 2; Length 1260;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 616 GTTGGAGAGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 675
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RESULT 14
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; Sequence 4, Application US/08447570
; Patent No. 5714589
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,570
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
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;; APPLICATION NUMBER: US 621,988
;; FILING DATE: 04-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 621,849
;; FILING DATE: 04-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 616,374
;; FILING DATE: 21-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 600,024
;; FILING DATE: 18-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 599,543
;; FILING DATE: 18-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 579,865
;; FILING DATE: 07-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 569,920
;; FILING DATE: 20-AUG-1990
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;; APPLICATION NUMBER: US 483,913
;; FILING DATE: 22-FEB-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 315,342
;; FILING DATE: 23-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 232,630
;; FILING DATE: 15-AUG-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 179,460
;; FILING DATE: 08-APR-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FITCHER, EDMUND R.
;; REGISTRATION NUMBER: 27,829
;; REFERENCE/DOCKET NUMBER: CRP-001CP6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/248-7000
;; TELEFAX: 617/248-7100
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1260 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHEetical: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: HOMO SAPIENS
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 9..1196
;; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
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US-08-447-570-4

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;; APPLICATION NUMBER: US 621,988
;; FILING DATE: 04-DEC-1990
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;; FILING DATE: 20-AUG-1990
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;; APPLICATION NUMBER: US 315,342
;; FILING DATE: 23-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 232,630
;; FILING DATE: 15-AUG-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 179,460
;; FILING DATE: 08-APR-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FITCHER, EDMUND R.
;; REGISTRATION NUMBER: 27,829
;; REFERENCE/DOCKET NUMBER: CRP-001CP6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/248-7000
;; TELEFAX: 617/248-7100
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1260 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHEtical: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: HOMO SAPIENS
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 9..1196
;; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
;; OTHER INFORMATION: /product= "CBMP2A"
;; OTHER INFORMATION: /note= "CBMP2A (CDNA)"
US-08-447-570-4

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RESULT 15
US-08-449-700-4
Sequence 4, Application US/08449700
Patent No. 5963758
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,700
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
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APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
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APPLICATION NUMBER: US 616,374
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FILING DATE: 18-OCT-1990
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FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: CDS
LOCATION: 9..1196
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US-08-449-700-4

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Best Local Similarity 99.8%; Pred. No. 0;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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3	1547	100.0	1547	6	US-10-139-814-1
4	1547	100.0	1547	6	US-10-366-345-10
5	1547	100.0	1547	6	US-10-295-027-159
6	1547	100.0	1547	7	US-10-302-812-19
7	1547	100.0	1547	7	US-10-283-975A-403
8	1547	100.0	1547	7	US-10-692-824-1
9	1547	100.0	1547	8	US-10-801-648-1
10	1547	100.0	1547	9	US-10-489-740-36
11	1547	100.0	1547	9	US-10-492-380-1
12	1547	100.0	1547	9	US-10-917-265-1
13	1547	100.0	1547	9	US-10-886-947-1
14	1547	100.0	1607	3	US-09-804-625-3
15	1547	100.0	1607	6	US-10-397-214-3
16	1547	100.0	1607	9	US-10-397-214-3
17	1545.4	99.9	1607	6	US-10-375-150-1
18	1314.8	85.0	2154	6	US-10-210-951-45
19	1314.8	85.0	2154	6	US-10-211-884-45
20	1314.8	85.0	2154	6	US-10-211-858-45
21	1227.2	79.3	1260	2	US-08-957-425-4
22	1227.2	79.3	1260	6	US-10-321-799-4
23	1227.2	79.3	1260	7	US-10-428-997A-4

24	1045.2	67.6	1314	3	US-09-935-144-39	Sequence 39, Appl
25	1026.2	66.3	1541	7	US-10-302-812-17	Sequence 17, Appl
26	896.6	58.0	1233	3	US-09-945-182-27	Sequence 27, Appl
27	896.6	58.0	1233	7	US-10-779-635-37	Sequence 27, Appl
28	880	56.9	14759	3	US-09-952-360-1	Sequence 1, Appl
29	880	56.9	14759	6	US-10-346-723-1	Sequence 1, Appl
30	880	56.9	173308	9	US-10-756-149-629	Sequence 629, App
31	576	37.2	576	6	US-10-029-386-20679	Sequence 20679, A
32	538	34.8	538	6	US-10-029-386-6968	Sequence 6968, Ap
33	440.2	28.5	508	3	US-09-918-995-21456	Sequence 21456, A
34	380.8	24.6	1432	9	US-10-169-050-63	Sequence 63, Appl
35	380.8	24.6	8611	9	US-10-169-050-17	Sequence 17, Appl
36	378	24.4	381	5	US-10-189-302-1	Sequence 1, Appl
37	378	24.4	381	7	US-10-354-856-1	Sequence 23, Appl
38	375	24.2	1400	7	US-10-302-812-23	Sequence 90, Appl
39	375	24.2	1569	6	US-10-264-049-90	Sequence 3, Appl
40	375	24.2	1751	5	US-10-189-302-3	Sequence 1309, Ap
41	375	24.2	1751	7	US-10-240-425-1309	Sequence 201, App
42	375	24.2	1751	8	US-10-278-698-201	Sequence 717, App
43	375	24.2	1751	8	US-10-278-698-717	Sequence 6, Appl
44	375	24.2	1788	2	US-08-957-425-6	Sequence 6, Appl
45	375	24.2	1788	6	US-10-321-799-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-044-716-1
; Sequence 1, Application US/10044716
; Publication No. US20020159986A1
; GENERAL INFORMATION:
; APPLICANT: LANGENFELD, John
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF CA
; FILE REFERENCE: 270/07005
; CURRENT APPLICATION NUMBER: US/10/044,716
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US60/261,252
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1547)
; OTHER INFORMATION: Homo sapiens: Taxon:9606
; NAME/KEY: gene
; LOCATION: (1)..(1547)
; OTHER INFORMATION: BMP2
; NAME/KEY: CDS
; LOCATION: (324)..(1514)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (429)..(1127)
; OTHER INFORMATION: Region: TGF-beta propeptide
; NAME/KEY: variation
; LOCATION: (432)..(432)
; OTHER INFORMATION: Allele = "T"; Allele = "G"
; NAME/KEY: variation
; LOCATION: (584)..(584)
; OTHER INFORMATION: Allele = "A"; Allele = "G"
; NAME/KEY: variation
; LOCATION: (893)..(893)
; OTHER INFORMATION: Allele = "T"; Allele = "A"
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor beta like domain
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGPB; Region: Transforming growth factor-beta (TGF-beta) family

US-10-044-716-1

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Query Match 100.0%; Score 1547; DB 5; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGGACTCTTGAACCTTGCAGGAGATAAATCTTGGCACCCCACTTTTGGCCGGTGCTT 60

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Qy 121 TGCCCGACACTGAGACGCTGTCTCCAGCTGTAAGAGAGAGACTGCGGCGCGGACCGG 180
Db 121 TGCCCGACACTGAGACGCTGTCTCCAGCTGTAAGAGAGAGACTGCGGCGCGGACCGG 180

Qy 181 GAGAAGGAGGAGGCAAGAAAAGAAACGACATTCGGTCTTGGCCAGAGTCCCTTTTGACC 240
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Qy 361 TTCCCGAGGCTCTCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 TTCCCGAGGCTCTCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

Qy 421 TCGCGCGCGCTGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
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Qy 601 CCGCGCCAGACACCGGTTGGAGGCGCAGCGCGGCAACACTGTGCGCAGCTTCC 660
Db 601 CCGCGCCAGACACCGGTTGGAGGCGCAGCGCGGCAACACTGTGCGCAGCTTCC 660

Qy 661 ACCATGAAGATCTTTGGAAGACTACAGAAACGAGTGGGAAAACACCGCGAGATTCT 720
Db 661 ACCATGAAGATCTTTGGAAGACTACAGAAACGAGTGGGAAAACACCGCGAGATTCT 720

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Db 721 TCTTTAATTTAAGTTCTATCCCGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780

Qy 781 TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAAATA 840
Db 781 TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAAATA 840

Qy 841 TTTATGAATCATATAAACCTGCAACAGCAACTCGAAATTCCTCGTGACCAAGATTTTGG 900
Db 841 TTTATGAATCATATAAACCTGCAACAGCAACTCGAAATTCCTCGTGACCAAGATTTTGG 900

Qy 901 ACACGAGTTGCTGAATCAGAACTCAAGCAGGTGGGAAAGTTTGTATGTCACCCCGCTG 960
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Qy 1141 GGCAATCTCTCCAAAGAGAAAAACGTCAAGCCAAACAACAACAGCGGAAACGCCTTA 1200
Db 1141 GGCAATCTCTCCAAAGAGAAAAACGTCAAGCCAAACAACAACAGCGGAAACGCCTTA 1200

Qy 1201 AGTCCAGCTCTTAAGAGACACCTTTGTACGTGGAATCTCAGTGAGCTGGGTGGATGACT 1260
Db 1201 AGTCCAGCTCTTAAGAGACACCTTTGTACGTGGAATCTCAGTGAGCTGGGTGGATGACT 1260

Qy 1261 GGATTTGGGTCCCGCGGGGTATCACGCTTTTACTGCCACGAGAAATGCCCTTTTCTC 1320
Db 1261 GGATTTGGGTCCCGCGGGGTATCACGCTTTTACTGCCACGAGAAATGCCCTTTTCTC 1320

Qy 1321 TGGCTGATCATCTGAACTCCACTAATCATGCCATTTGTTTCAAGCGTTGGTCAACTCTGTTA 1380
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Qy 1381 ACTTAAGATTCCTTAAGGCAATGCTGTGCTCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
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Db 1441 ACCTTGACGAGAAATGAAAAGCTTGTATTAAAGAACTATCAGGACATGTTGTGAGAGGTT 1500

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Db 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATAATACATAATATATATA 1547
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US-10-286-152A-1
; Sequence 1, Application US/10286152A
; Publication No. US20030134308A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Research, Ltd.
; TITLE OF INVENTION: Bone Morphogenic Proteins (BMP), BMP Receptors and BMP Binding Pr
; FILE REFERENCE: 2312 US
; CURRENT APPLICATION NUMBER: US/10/286,152A
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-286-152A-1
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Query Match 100.0%; Score 1547; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGGGACTCTTGAACCTTGCAGGAGATAAATCTTGGCACCCCACTTTTGGCCGGTGCTT 60
Db 1 GGGGACTCTTGAACCTTGCAGGAGATAAATCTTGGCACCCCACTTTTGGCCGGTGCTT 60

Qy 61 TGCCCGACGCGAGCTGTCTCGCCATCTCCGAGCCCAACGCGCCCTCCACTCTCCGCGCT 120
Db 61 TGCCCGACGCGAGCTGTCTCGCCATCTCCGAGCCCAACGCGCCCTCCACTCTCCGCGCT 120

Qy 121 TGCCCGACACTGAGACGCTGTTCACGCGTGAAGAGAGAGACTGCGCGCGGCAACCGG 180
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US-10-139-814-1
 ; Sequence 1, Application US/10139814
 ; Publication No. US20030134790A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Langenfeld, John
 ; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF
 ; TITLE OF INVENTION: CANCER
 ; FILE REFERENCE: 273/136 Michael J. Wise
 ; CURRENT APPLICATION NUMBER: US/10/139,814
 ; PRIOR FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: US60/261,252
 ; PRIOR FILING DATE: 2001-01-12
 ; PRIOR APPLICATION NUMBER: US10/044,716
 ; PRIOR FILING DATE: 2002-01-11
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1547
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
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 ; NAME/KEY: source
 ; LOCATION: (1)..(1547)
 ; OTHER INFORMATION: Homo sapiens: Taxon:9606
 ; FEATURE:
 ; NAME/KEY: Gene
 ; LOCATION: (1)..(1547)
 ; OTHER INFORMATION: BMP2
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (324)..(1514)
 ; OTHER INFORMATION:
 ; FEATURE:
 ; NAME/KEY: misc feature
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 ; OTHER INFORMATION: Region: TGF-beta propeptide
 ; FEATURE:
 ; NAME/KEY: variation
 ; LOCATION: (432)..(432)
 ; OTHER INFORMATION: Allele = "T"; Allele = "G"
 ; FEATURE:
 ; NAME/KEY: variation
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 ; OTHER INFORMATION: Allele = "T"; Allele = "A"
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 ; LOCATION: (1205)..(1511)

OTHER INFORMATION: TGF-beta; Region: Transforming growth factor beta like domain
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGFb; Region: Transforming growth factor-beta (TGF-beta) family
US-10-139-814-1

Query Match 100.0%; Score 1547; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 421 TCGCGGCGCGCTGCTGCGGCGCGCGCTCATCCAGCCCTCTGAAGAGTCTGAGCGAGT 480
Db 421 TCGCGGCGCGCTGCTGCGGCGCGCGCTCATCCAGCCCTCTGAGCGAGTCTGAGCGAGT 480
Qy 481 TCGAGTTGCGGCTCTCAGCATGTTTCCGCTGAAACAGAGACCCACCCAGCAGGAGCG 540
Db 481 TCGAGTTGCGGCTCTCAGCATGTTTCCGCTGAAACAGAGACCCACCCAGCAGGAGCG 540
Qy 541 CCGTGTGCCCCCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGCGGCTCAC 600
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Db 961 TGATCGCGTGGACTGCAACAGGACACGCCAACCAATGATTCGTGGTGAAGTGGCCACT 1020
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RESULT 4
US-10-366-345-10
; Sequence 10, Application US/10366345
; Publication No. US20030224501A1
; GENERAL INFORMATION:
; APPLICANT: Young, et al.
; TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT189
; CURRENT APPLICATION NUMBER: US/10/366,345
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-366-345-10

Query Match 100.0%; Score 1547; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTCTTTGAACCTTGACGGAGAAATACTTGCGCACCCCACTTTGCGCGGCTGCTT 60
Db 1 GGGGACTCTTTGAACCTTGACGGAGAAATACTTGCGCACCCCACTTTGCGCGGCTGCTT 60
Qy 61 TGCCCCAGCGAGCGCTGCTTCCGCACTTCGAGAGCCCAACCGCCCTCACTCTCGGCT 120
Db 61 TGCCCCAGCGAGCGCTGCTTCCGCACTTCGAGAGCCCAACCGCCCTCACTCTCGGCT 120

QY 121 TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGGACCCCGG 180
DB 121 TGCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGGACCCCGG 180
QY 181 GAG 240
DB 181 GAG 240
QY 241 AGAGTTTTCATGATGAG 300
DB 241 AGAGTTTTCATGATGAG 300
QY 301 CTGCGGCTCTCTAAAGGTGAGACATGAGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 CTGCGGCTCTCTAAAGGTGAGACATGAGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 TTCCCGAGGCTCTCTGAGGAG 420
DB 361 TTCCCGAGGCTCTCTGAGGAG 420
QY 421 TCGCGGCGGCTCTGAGGAG 480
DB 421 TCGCGGCGGCTCTGAGGAG 480
QY 481 TCGAGTTGCGGCTCTGAGGAG 540
DB 481 TCGAGTTGCGGCTCTGAGGAG 540
QY 541 CCGTGGTGGGCTCTGAGGAG 600
DB 541 CCGTGGTGGGCTCTGAGGAG 600
QY 601 CCGGCGGAG 660
DB 601 CCGGCGGAG 660
QY 661 ACCATGAG 720
DB 661 ACCATGAG 720
QY 721 TCTTTAAATTAAGTTCTATCCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 TCTTTAAATTAAGTTCTATCCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 TCCGAG 840
DB 781 TCCGAG 840
QY 841 TTTATGAATCATATAAAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 TTTATGAATCATATAAAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 ACACGAGTTGGTGAATCAG 960
DB 901 ACACGAGTTGGTGAATCAG 960
QY 961 TGAATGAGTTGGTGAATCAG 1020
DB 961 TGAATGAGTTGGTGAATCAG 1020
QY 1021 TGGAG 1080
DB 1021 TGGAG 1080
QY 1081 ATGAACACAGCTGGTTCACAG 1140
DB 1081 ATGAACACAGCTGGTTCACAG 1140
QY 1141 GGCATCTCTCCACAAAG 1200
DB 1141 GGCATCTCTCCACAAAG 1200

QY 1201 AGTCCAGCTGTAAGAGACACCTTTGTACGTGGAGCTTCAAGTGAAGTGGGGTGGAAATGACT 1260
DB 1201 AGTCCAGCTGTAAGAGACACCTTTGTACGTGGAGCTTCAAGTGAAGTGGGGTGGAAATGACT 1260
QY 1261 GGATTTGGCTCCCGGGGTATCAGCGCTTTTACTGCCACGGAGAGATGCCCTTTTCCCTC 1320
DB 1261 GGATTTGGCTCCCGGGGTATCAGCGCTTTTACTGCCACGGAGAGATGCCCTTTTCCCTC 1320
QY 1321 TGGCTGATCATCTGAACTCCCACTAATCATGTCATTTGTTTTCAGACGTTGCTCAACTCTGTTA 1380
DB 1321 TGGCTGATCATCTGAACTCCCACTAATCATGTCATTTGTTTTCAGACGTTGCTCAACTCTGTTA 1380
QY 1381 ACTTAAGATCTTAAAGCATGCTGTCCTCCGACAGAACTCAGTCTATCTCGATGCTGT 1440
DB 1381 ACTTAAGATCTTAAAGCATGCTGTCCTCCGACAGAACTCAGTCTATCTCGATGCTGT 1440
QY 1441 ACCTTGACGAGAGTGAAGAGTTGTTTAAAGAACTATCAGGACATGTTGAGAGGTT 1500
DB 1441 ACCTTGACGAGAGTGAAGAGTTGTTTAAAGAACTATCAGGACATGTTGAGAGGTT 1500
QY 1501 GTGGTGTGCTAGTACAGCAAAATTAATAACATAAATATATATA 1547
DB 1501 GTGGTGTGCTAGTACAGCAAAATTAATAACATAAATATATATA 1547

RESULT 5

US-10-295-027-159
; Sequence 159, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glyne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-159

Query Match		100.0%;	Score 1547;	DB 6;	Length 1547;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches 1547;		Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
Qy	1	GGGACTCTTTGAATCTGACGGAGATAAATCTTGGCACCCACCTTTTGGCGCGGTGCTT	60			
Db	1	GGGACTCTTTGAATCTGACGGAGATAAATCTTGGCACCCACCTTTTGGCGCGGTGCTT	60			
Qy	61	TGCCCCAGCGAGCGCTTCCGCAATCTCCGAGCCCCACCGCCCTCCACTCTCGGCT	120			
Db	61	TGCCCCAGCGAGCGCTTCCGCAATCTCCGAGCCCCACCGCCCTCCACTCTCGGCT	120			
Qy	121	TGCCCCGACACTGAGACGCTGTCCAGCTGAAAGAGAGACTGCGGCGCGGACCCGG	180			
Db	121	TGCCCCGACACTGAGACGCTGTCCAGCTGAAAGAGAGACTGCGGCGCGGACCCGG	180			
Qy	181	GAGAGGAGGAGGCAAGAAAGAAAGCAATTCGGTCTTGGCCAGGTCCTTTTGACC	240			
Db	181	GAGAGGAGGAGGCAAGAAAGAAAGCAATTCGGTCTTGGCCAGGTCCTTTTGACC	240			
Qy	241	AGAGTTTTCATGTGACGCTCTTTCAATGGAGCTGTCCCGGCTCTTCTTAGACGA	300			
Db	241	AGAGTTTTCATGTGACGCTCTTTCAATGGAGCTGTCCCGGCTCTTCTTAGACGA	300			
Qy	301	CTCGGCTCTCTAAAGTTCGACCAATGTTGGCGGGACCGGCTGTCTTAGCGTGTCTGC	360			
Db	301	CTCGGCTCTCTAAAGTTCGACCAATGTTGGCGGGACCGGCTGTCTTAGCGTGTCTGC	360			
Qy	361	TTCCCCAGGCTCTCTCGGCGGGCGGCTGGCTCTGTTCCGGAGCTGGCGCGGAGAGT	420			
Db	361	TTCCCCAGGCTCTCTCGGCGGGCGGCTGGCTCTGTTCCGGAGCTGGCGCGGAGAGT	420			
Qy	421	TCGCGGCGGCGCTCGTGGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT	480			
Db	421	TCGCGGCGGCGCTCGTGGGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT	480			
Qy	481	TCGAGTTGCGGCTGTGACGATGTTCCGCTGAAACAGAGACCCACCCGAGGAGAGC	540			
Db	481	TCGAGTTGCGGCTGTGACGATGTTCCGCTGAAACAGAGACCCACCCGAGGAGAGC	540			
Qy	541	CCGTGGTCCGCCCTACATGCTAGACCTGTATCGCAGGACCTCAGCTCAGCGGGCTCAC	600			
Db	541	CCGTGGTCCGCCCTACATGCTAGACCTGTATCGCAGGACCTCAGCTCAGCGGGCTCAC	600			
Qy	601	CCGCCCCAGACCA CGGTTGAGAGGGCAGCCAGCCGAGCCCAACTGTGGCGAGCTTCC	660			
Db	601	CCGCCCCAGACCA CGGTTGAGAGGGCAGCCAGCCGAGCCCAACTGTGGCGAGCTTCC	660			
Qy	661	ACCATGAAGATCTTTGGAGAACTACCAAGAAACGAGTGGGAAACAAACCCGAGATCT	720			
Db	661	ACCATGAAGATCTTTGGAGAACTACCAAGAAACGAGTGGGAAACAAACCCGAGATCT	720			
Qy	721	TCCTTAATTTAAGTTCTATCCCGAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTT	780			
Db	721	TCCTTAATTTAAGTTCTATCCCGAGGAGGTTTATCACTCAGCAGAGCTTCAGGTTT	780			
Qy	781	TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA	840			
Db	781	TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATA	840			
Qy	841	TTTATGAATCATTAACCTGCAACAGCAACTCGAAATTCCTGTCAGCAGACTTTTGG	900			
Db	841	TTTATGAATCATTAACCTGCAACAGCAACTCGAAATTCCTGTCAGCAGACTTTTGG	900			
Qy	901	ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTG	960			
Db	901	ACACAGGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTG	960			
Qy	961	TGATCCGGTGGATGCA CAGGAGACCGCCAAACCAATGGAATTCGTGGTGAAGTGGCCACT	1020			
Db	961	TGATCCGGTGGATGCA CAGGAGACCGCCAAACCAATGGAATTCGTGGTGAAGTGGCCACT	1020			

Qy	1021	TGGAGGAGAAACRAGGTGTCTCAAGAGACATGTTAGGATAAGCAGGTCTTTGCCACCAAG	1080			
Db	1021	TGGAGGAGAAACRAGGTGTCTCAAGAGACATGTTAGGATAAGCAGGTCTTTGCCACCAAG	1080			
Qy	1081	ATGAACACAGCTGTGTACAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAAAG	1140			
Db	1081	ATGAACACAGCTGTGTACAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAAAG	1140			
Qy	1141	GGCATCTCTTCCACAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAAGCGCTTAA	1200			
Db	1141	GGCATCTCTTCCACAAAGAGAAAACGTCAGGCCAAACACAAACAGCGGAAAGCGCTTAA	1200			
Qy	1201	AGTCCAGCTGTAGAGACACCCCTTTGTACGTGGACTTTCAGTGAGCTGGGTGGGAATGACT	1260			
Db	1201	AGTCCAGCTGTAGAGACACCCCTTTGTACGTGGACTTTCAGTGAGCTGGGTGGGAATGACT	1260			
Qy	1261	GGATTGTGGTCCCGCGGGGTATCACGCTTTTACTGCCACGGAGAAATGCCCTTTTCTCTC	1320			
Db	1261	GGATTGTGGTCCCGCGGGGTATCACGCTTTTACTGCCACGGAGAAATGCCCTTTTCTCTC	1320			
Qy	1321	TGGCTGATCATCTGAACTCACTAAATCATGCTCAATTTACTGCCACGGAGAAATGCCCTTTCTGTTA	1380			
Db	1321	TGGCTGATCATCTGAACTCACTAAATCATGCTCAATTTACTGCCACGGAGAAATGCCCTTTCTGTTA	1380			
Qy	1381	ACTCTAAGATTCCTAAGCGCATGCTGTCCCGCAGAACTCAGTGCTATCTCGATGCTGT	1440			
Db	1381	ACTCTAAGATTCCTAAGCGCATGCTGTCCCGCAGAACTCAGTGCTATCTCGATGCTGT	1440			
Qy	1441	ACCTTGACGAGAAATGAAAAGGTTGTATTAAGAACTATCAGGACATGTGTTGTGAGGGTT	1500			
Db	1441	ACCTTGACGAGAAATGAAAAGGTTGTATTAAGAACTATCAGGACATGTGTTGTGAGGGTT	1500			
Qy	1501	GTGGGTCTGCTAGTACAGCAAAATTAATAATACATAATATATATA 1547				
Db	1501	GTGGGTCTGCTAGTACAGCAAAATTAATAATACATAATATATATA 1547				

RESULT 6
US-10-302-812-19
; Sequence 19, Application US/10302812
; Publication No. US20040087016A1
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND
; FILE REFERENCE: HYDR-P02-004
; CURRENT APPLICATION NUMBER: US/10/302,812
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-302-812-19

Query Match		100.0%;	Score 1547;	DB 7;	Length 1547;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches 1547;		Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
Qy	1	GGGAGCTTCTTGAACCTTGCAGGGAGATAAATCTTGGCACCCACCTTTTGGCGCGGTGCTT	60			
Db	1	GGGAGCTTCTTGAACCTTGCAGGGAGATAAATCTTGGCACCCACCTTTTGGCGCGGTGCTT	60			
Qy	61	TGCCCCAGCGAGCGCTCTTCCGCAATCTCCGAGCCCCACCGCCCTCCACTCTCGGCT	120			
Db	61	TGCCCCAGCGAGCGCTCTTCCGCAATCTCCGAGCCCCACCGCCCTCCACTCTCGGCT	120			
Qy	121	TGCCCCGACACTGAGACGCTGTTCAGCGTGAAGAGAGACTGCGGCGCGGACCCGG	180			
Db	121	TGCCCCGACACTGAGACGCTGTTCAGCGTGAAGAGAGACTGCGGCGCGGACCCGG	180			
Qy	181	GAGAGGAGGAGGCAAGAAAGAAAGGAACTTCGTGGTCTTGGCGCAGGTCTTTTGACC	240			

361 TTCCCCAGGTCCTCTCGGCGCGCGGCTGCTGCTCCGAGCTGGCGCGCAGGAAGT 420
Db |||||
361 TTCCCCAGGTCCTCTCGGCGCGCGGCTGCTGCTCCGAGCTGGCGCGCAGGAAGT 420
Qy |||||
421 TCGGCGGCGGCTCGTTCGGGCGCGCCCTCATCCAGCCCTCTGAGCAGGTCCTGAGCGAGT 480
Db |||||
421 TCGGCGGCGGCTCGTTCGGGCGCGCCCTCATCCAGCCCTCTGAGCAGGTCCTGAGCGAGT 480
Qy |||||
481 TCGAGTTTCGGCTGCTCAGCATGTTTCGGCTTGAACACAGAGACCCACCCCGCAGCGGACG 540
Db |||||
481 TCGAGTTTCGGCTGCTCAGCATGTTTCGGCTTGAACACAGAGACCCACCCCGCAGCGGACG 540
Qy |||||
541 CCGTGTGTCGCCCTTACATGCTAGACCTGTATCGCAGGCACTCAGCTCAGCGCGGCTCAC 600
Db |||||
541 CCGTGTGTCGCCCTTACATGCTAGACCTGTATCGCAGGCACTCAGCTCAGCGCGGCTCAC 600
Qy |||||
601 CCGCCCCAGACCCCGGTTGAGAGGGCAGCCAGCCGAGCCCACTGTGCGCAGCTTCC 660
Db |||||
601 CCGCCCCAGACCCCGGTTGAGAGGGCAGCCAGCCGAGCCCACTGTGCGCAGCTTCC 660
Qy |||||
661 ACCATGAAGATCTTTGGAAGAACTACAGAGAAACGAGTGGGAAACAAACCCGGAGATTCT 720
Db |||||
661 ACCATGAAGATCTTTGGAAGAACTACAGAGAAACGAGTGGGAAACAAACCCGGAGATTCT 720
Qy |||||
721 TCTTTAATTTAAGTTCTATCCCGCAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db |||||
721 TCTTTAATTTAAGTTCTATCCCGCAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Qy |||||
781 TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCAGATTAAATA 840
Db |||||
781 TCCGAGAACAGATGCAAGATCTTTAGGAAACAATAGCAGTTTCCATCACCAGATTAAATA 840
Qy |||||
841 TTTATGAATCATTAACCTGCAACAGCCAACTCGAAATCCCGTGCACAGACTTTTGG 900
Db |||||
841 TTTATGAATCATTAACCTGCAACAGCCAACTCGAAATCCCGTGCACAGACTTTTGG 900
Qy |||||
901 ACACAGGTTGCTGAATCAGAACTCAAGCAGTGGGAAAGTTTGTGTCACCCCGCTG 960
Db |||||
901 ACACAGGTTGCTGAATCAGAACTCAAGCAGTGGGAAAGTTTGTGTCACCCCGCTG 960
Qy |||||
961 TGATGCGGTGACTGCAACAGGACACGCAACCATGATGATTCGTGTGGAAGTGCCCACT 1020
Db |||||
961 TGATGCGGTGACTGCAACAGGACACGCAACCATGATGATTCGTGTGGAAGTGCCCACT 1020
Qy |||||
1021 TGGAGGAGAAACAAGTGTCTCCAGAGACATGTTAGGATGAGCAGGTCCTTTGACCAAG 1080
Db |||||
1021 TGGAGGAGAAACAAGTGTCTCCAGAGACATGTTAGGATGAGCAGGTCCTTTGACCAAG 1080
Qy |||||
1081 ATGAACACAGCTGGTACAGATAGGCCATTTAGTAACTTTTGGCCATGATGGAAG 1140
Db |||||
1081 ATGAACACAGCTGGTACAGATAGGCCATTTAGTAACTTTTGGCCATGATGGAAG 1140
Qy |||||
1141 GGCACTCTCTCCACAAAGAGAGAAACGTCAGGCCAAACACAAACAGCGGAAACGCCCTTA 1200
Db |||||
1141 GGCACTCTCTCCACAAAGAGAGAAACGTCAGGCCAAACACAAACAGCGGAAACGCCCTTA 1200
Qy |||||
1201 AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGAATTCAGTGAGCGTGGGTTGAATGACT 1260
Db |||||
1201 AGTCAGCTGTAAGAGACACCCCTTTGTACGTGGAATTCAGTGAGCGTGGGTTGAATGACT 1260
Qy |||||
1261 GGATTTGGCTCCCGGGGTATCAGCCTTTTACTGTCACGGAGATGCCCTTTTCTC 1320
Db |||||
1261 GGATTTGGCTCCCGGGGTATCAGCCTTTTACTGTCACGGAGATGCCCTTTTCTC 1320
Qy |||||
1321 TGGCTGATCATCTGAACCTCCACTAATCATGCCATTTGTTACAGCGTTGTCACCTCTGTTA 1380
Db |||||
1321 TGGCTGATCATCTGAACCTCCACTAATCATGCCATTTGTTACAGCGTTGTCACCTCTGTTA 1380
Qy |||||
1381 ACTTAAGATTCCTAAGGATGCTGTGTCGCCAGAGAACTCAGTGCTATCTCGATGCTGT 1440
Db |||||
1381 ACTTAAGATTCCTAAGGATGCTGTGTCGCCAGAGAACTCAGTGCTATCTCGATGCTGT 1440
Qy |||||
1441 ACCTTGACGAGATGAAAAGTGTGTTAAGAACTATCAGGACATGTTGTGAGGGGTT 1500

Db ||||| 1441 ACCTTGACGAGATGAAAAGTGTGTTAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Qy ||||| 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATACATAAATATATATA 1547
Db ||||| 1501 GTGGGTGCTGCTAGTACAGCAAAATTAATACATAAATATATATA 1547
RESULT 8
US-10-692-824-1
; Sequence 1, Application US/10692824
; Publication No. US20040126375A1
; GENERAL INFORMATION:
; APPLICANT: Langenfeld, John
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 54704.8036.US03
; CURRENT APPLICATION NUMBER: US/10/692,824
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US60/261,252
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US10/044,716
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1547)
; OTHER INFORMATION: Homo sapiens: Taxon:9606
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1547)
; OTHER INFORMATION: BMP2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (324)..(1514)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (429)..(1127)
; OTHER INFORMATION: Region: TGF-beta propeptide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (432)..(432)
; OTHER INFORMATION: Allele = "T"; Allele = "G"
; FEATURE:
; NAME/KEY: variation
; LOCATION: (584)..(584)
; OTHER INFORMATION: Allele = "A"; Allele = "G"
; FEATURE:
; NAME/KEY: variation
; LOCATION: (893)..(893)
; OTHER INFORMATION: Allele = "T"; Allele = "A"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor beta like domain
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor-beta (TGF-beta) family
US-10-692-824-1
Query Match 100.0%; Score 1547; DB 7; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTGAACCTTGCAGGGAGAAATACTTGCACACCCCACTTTGCGCGGTCCTT 60
Db 1 GGGGACTTCTTGAACCTTGCAGGGAGAAATACTTGCACACCCCACTTTTGGCGCGGTCCTT 60

Db 181 GAGAAAGGAGGAGGCAAGAAAGAAAGGAAACGGACATTCGGTCCCTTGCGCCAGGTCCTTTTGACC 240
Qy 241 AGAGTTTTTCAATGTGGACGCTCTTTCAATGGAGCGTGTCCCGCGTGTCTTTAGACGGA 300
Db 241 AGAGTTTTTCAATGTGGACGCTCTTTCAATGGAGCGTGTCCCGCGTGTCTTTAGACGGA 300
Qy 301 CTGCGGTCTCTAAAGGTCGACACCATGTGTGGCGGGACCCCGTGTCTTTCTAGCGTTGCTGC 360
Db 301 CTGCGGTCTCTAAAGGTCGACACCATGTGTGGCGGGACCCCGTGTCTTTCTAGCGTTGCTGC 360
Qy 361 TTCCCGCAGGTCTCTCTGCGCGCGCGGCTGGCTCTGTTCCGAGAGTGGCGCGCAGGAAGT 420
Db 361 TTCCCGCAGGTCTCTCTGCGCGCGCGGCTGGCTCTGTTCCGAGAGTGGCGCGCAGGAAGT 420
Qy 421 TCGCGCGCGGCTGTGTGGCGCGCGGCTGTATCCAGACCTCTGACGAGTCTTGAGCGAGT 480
Db 421 TCGCGCGCGGCTGTGTGGCGCGCGGCTGTATCCAGACCTCTGACGAGTCTTGAGCGAGT 480
Qy 481 TCGAGTTGCGGCTGTCTAGCATGTTCGGCTGAAACAGAGACCCACCCAGCAGGGACG 540
Db 481 TCGAGTTGCGGCTGTCTAGCATGTTCGGCTGAAACAGAGACCCACCCAGCAGGGACG 540
Qy 541 CCGTGGTCCCGCTTACATGTAGACCTGTATCGCAGGCACTCAGGTGAGCGCGGCTCAC 600
Db 541 CCGTGGTCCCGCTTACATGTAGACCTGTATCGCAGGCACTCAGGTGAGCGCGGCTCAC 600
Qy 601 CCGCGCCAGACACCGTTGAGAGGGCAGCCAGCGAGCCAAACATGTGGGAGCTTCC 660
Db 601 CCGCGCCAGACACCGTTGAGAGGGCAGCCAGCGAGCCAAACATGTGGGAGCTTCC 660
Qy 661 ACCATGAGAGATCTTTGGAAGATACACAGAAACGAGTGGGAAACACACCGGAGATTCT 720
Db 661 ACCATGAGAGATCTTTGGAAGATACACAGAAACGAGTGGGAAACACACCGGAGATTCT 720
Qy 721 TCTTTAATTTAAGTTCTATCCCGCAGGAGGATTTATCACTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAATTTAAGTTCTATCCCGCAGGAGGATTTATCACTCAGCAGAGCTTCAGGTTT 780
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCAATCCCGAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCAATCCCGAATTAATA 840
Qy 841 TTTTGAATCATATAAACCTGCAACAGCAACTCGAATTCGCCGTGACCAAGCTTTTGG 900
Db 841 TTTTGAATCATATAAACCTGCAACAGCAACTCGAATTCGCCGTGACCAAGCTTTTGG 900
Qy 901 ACAACAGGTTGGTGAATCAGAGATGCAAGCAGGTGGGAAAGTTTGAATGTCACCCCGCTG 960
Db 901 ACAACAGGTTGGTGAATCAGAGATGCAAGCAGGTGGGAAAGTTTGAATGTCACCCCGCTG 960
Qy 961 TGATCGGTGGAATGCAACAGGGAACCGCAACCATAGGATTCGTGGTGGAAAGTGCCCACT 1020
Db 961 TGATCGGTGGAATGCAACAGGGAACCGCAACCATAGGATTCGTGGTGGAAAGTGCCCACT 1020
Qy 1021 TGGAGGAGAAACAGGTGTCTCCAGAGACATGTTAGGATAGCAGGTCTTTGACCCAG 1080
Db 1021 TGGAGGAGAAACAGGTGTCTCCAGAGACATGTTAGGATAGCAGGTCTTTGACCCAG 1080
Qy 1081 ATGAACACAGCTGGTCAAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAAG 1140
Db 1081 ATGAACACAGCTGGTCAAGATAAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAAG 1140
Qy 1141 GGCAATCTCTCAAAAAAGAGAAACCGTCAAGGCCAAACACAAACAGCGGAAACGCCCTTA 1200
Db 1141 GGCAATCTCTCAAAAAAGAGAAACCGTCAAGGCCAAACACAAACAGCGGAAACGCCCTTA 1200
Qy 1201 AGTCAGCTGTGAAGAGACACCTTTGTAGCTGGACTTCAGTGAGTGGGGTGGATGACT 1260
Db 1201 AGTCAGCTGTGAAGAGACACCTTTGTAGCTGGACTTCAGTGAGTGGGGTGGATGACT 1260
Qy 1261 GGATTTGGCTCCCGCGGGTATCACGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1320
Db 1261 GGATTTGGCTCCCGCGGGTATCACGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTC 1320

RESULT 10

US-10-489-740-36
; Sequence 36, Application US/10489740
; Publication No. US20050112574A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: P9
; FILE REFERENCE: Angiogenesis_PCT
; CURRENT APPLICATION NUMBER: US/10/489,740
; CURRENT FILING DATE: 2004-03-15
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-489-740-36

Query Match 100.0%; Score 1547; DB 9; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGACTCTTTGAACCTTGCAGGGAGAAATAACTTCGCACACCCCACTTTTGGCGCGGTGCCTT 60
Db 1 GGGGACTCTTTGAACCTTGCAGGGAGAAATAACTTCGCACACCCCACTTTTGGCGCGGTGCCTT 60
Qy 61 TGCCCCAGCGGAGCCTGTTCGCCATCTCGAGAGCCCAACCGCCCTTCCAATCTTCGGCT 120
Db 61 TGCCCCAGCGGAGCCTGTTCGCCATCTCGAGAGCCCAACCGCCCTTCCAATCTTCGGCT 120
Qy 121 TGCCCCGACACTGAGACGCTGTTCACGCTGAAAGAGAGACTCGCGGCGCGGACCCCGG 180
Db 121 TGCCCCGACACTGAGACGCTGTTCACGCTGAAAGAGAGACTCGCGGCGCGGACCCCGG 180
Qy 181 GAGAAAGGAGGAGGCAAGAAAGGAAACGGACATTCGGTTCCTTGGCCAGAGTCTCTTGACC 240
Db 181 GAGAAAGGAGGAGGCAAGAAAGGAAACGGACATTCGGTTCCTTGGCCAGAGTCTCTTGACC 240
Qy 241 AGAGTTTTTCAATGTGACGCTCTTTCAATGGACGCTGTCCCGCGTGTCTTTAGACGGA 300
Db 241 AGAGTTTTTCAATGTGACGCTCTTTCAATGGACGCTGTCCCGCGTGTCTTTAGACGGA 300
Qy 301 CTGCGGTCTCTTAAGGTTCGACCATGTGTGGCGGGACCCCGTGTCTTCTAGCGTTGCTGC 360
Db 301 CTGCGGTCTCTTAAGGTTCGACCATGTGTGGCGGGACCCCGTGTCTTCTAGCGTTGCTGC 360
Qy 361 TTCCCGCAGGTCTCTCTGCGCGCGCGGCTGGCTCTGTTCCGAGAGTGGCGCGCAGGAAGT 420
Db 361 TTCCCGCAGGTCTCTCTGCGCGCGCGGCTGGCTCTGTTCCGAGAGTGGCGCGCAGGAAGT 420
Qy 421 TCGCGCGCGGCTGTGTGGCGCGCGGCTGTATCCAGACCTCTGACGAGTCTTGAGCGAGT 480
Db 421 TCGCGCGCGGCTGTGTGGCGCGCGGCTGTATCCAGACCTCTGACGAGTCTTGAGCGAGT 480
Qy 481 TCGAGTTGCGGCTGTCTAGCATGTTCGGCTGAAACAGAGACCCACCCAGCAGGGACG 540

481 TCAGTTGCGGTGCTCAGCATGTTTCGGCTGAAACACAGAGACCCACCCAGCAGGAGC 540
541 CGGTGGTGGCCCTTACATGCTAGACCTGTATCGCAGGACCTCAGGTGAGCGGGCTCAC 600
541 CGGTGGTGGCCCTTACATGCTAGACCTGTATCGCAGGACCTCAGGTGAGCGGGCTCAC 600
601 CGCGCCCAAGACACCGGTTGGAGAGGGCAGCCAGCGAGCCAACTGTGGCAGCTTCC 660
601 CGCGCCCAAGACACCGGTTGGAGAGGGCAGCCAGCGAGCCAACTGTGGCAGCTTCC 660
661 ACCATGAAGAATCTTTTGAAGAACTTACAGAAACAGAGTGGGAAACAAACCGGAGATTCT 720
661 ACCATGAAGAATCTTTTGAAGAACTTACAGAAACAGAGTGGGAAACAAACCGGAGATTCT 720
721 TCTTTAAATTTAAGTTCTATCCCAAGGAGGAGTTTATCACCCTCAGCAGAGCTTCAGGTTT 780
721 TCTTTAAATTTAAGTTCTATCCCAAGGAGGAGTTTATCACCCTCAGCAGAGCTTCAGGTTT 780
781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAAATTAATA 840
781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAAATTAATA 840
841 TTTATGAATATCAATAAACTGCAACAGCCAACTCGAAATTCGCCGTGACAGACTTTTGG 900
841 TTTATGAATATCAATAAACTGCAACAGCCAACTCGAAATTCGCCGTGACAGACTTTTGG 900
901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTTCATGTACCCCGGTG 960
901 ACACAGGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTTCATGTACCCCGGTG 960
961 TGATCGGTGGATCTCACAGGAGACACGCCAACATGGAATTCGTGTGGAAGTGGCCCACT 1020
961 TGATCGGTGGATCTCACAGGAGACACGCCAACATGGAATTCGTGTGGAAGTGGCCCACT 1020
1021 TGGAGGAGAAACAAGGTGTCTCAAGAGACATGTTAGGATAGCAGGTCTTTTGACCCAAG 1080
1021 TGGAGGAGAAACAAGGTGTCTCAAGAGACATGTTAGGATAGCAGGTCTTTTGACCCAAG 1080
1081 ATGAACACAGCTGGTACAGATAGGCCATTCCTAGTAACATTTTGGCCATGATGAAAG 1140
1081 ATGAACACAGCTGGTACAGATAGGCCATTCCTAGTAACATTTTGGCCATGATGAAAG 1140
1141 GGCATCCTCTCCACAAAGAGAAACGTCAGGACCAACACAAACAGCGGAAACGCTTA 1200
1141 GGCATCCTCTCCACAAAGAGAAACGTCAGGACCAACACAAACAGCGGAAACGCTTA 1200
1201 AGTCAGCTGTAAAGACACACCTTTTGTACGTGGAATTCAGTGACGTGGGTGGAATGACT 1260
1201 AGTCAGCTGTAAAGACACACCTTTTGTACGTGGAATTCAGTGACGTGGGTGGAATGACT 1260
1261 GGAATGTGGCTCCCGGGGTATCAGCCTTTTACTGCAACAGGAGATGCGCCTTTTCCTC 1320
1261 GGAATGTGGCTCCCGGGGTATCAGCCTTTTACTGCAACAGGAGATGCGCCTTTTCCTC 1320
1321 TGGCTGATCATCTGAACCTCACTAATCATGCCATGTCATGTCAGACGTGGTCAACTCTGTTA 1380
1321 TGGCTGATCATCTGAACCTCACTAATCATGCCATGTCATGTCAGACGTGGTCAACTCTGTTA 1380
1381 ACTCTAAGATTCCTAAGGATGCTGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
1381 ACTCTAAGATTCCTAAGGATGCTGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGT 1440
1441 ACCTTACAGAGATGAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGGAGGTT 1500
1441 ACCTTACAGAGATGAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGGAGGTT 1500
1501 GTGGGTGCTGTAGTACGCAAAATTAATACATAAATATATATA 1547
1501 GTGGGTGCTGTAGTACGCAAAATTAATACATAAATATATATA 1547

US-10-492-380-1
; Sequence 1, Application US/10492380
; Publication No. US2005011858A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Research, Ltd.
; APPLICANT: Clark, Abbot P.
; TITLE OF INVENTION: Bone Morphogenic Proteins (BMP), BMP Receptors and BMP Binding
; TITLE OF INVENTION: Proteins and Their Use in the Diagnosis and Treatment of Glaucom
; FILE REFERENCE: 2312 US
; CURRENT APPLICATION NUMBER: US/10/492,380
; CURRENT FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-492-380-1

Query Match 100.0%; Score 1547; DB 9; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTCTTGAATCTGACGGAGAAATACTTGGGCAACCCACTTTTGGCGGTCGCTT 60
DB 1 GGGGACTTCTTGAATCTGACGGAGAAATACTTGGGCAACCCACTTTTGGCGGTCGCTT 60
QY 61 TGCCCCCAGCGAGCTGCTTCGCCATCTCCGAGCCGCCACCGCCCTCCACTCCCTGGGCT 120
DB 61 TGCCCCCAGCGAGCTGCTTCGCCATCTCCGAGCCGCCACCGCCCTCCACTCCCTGGGCT 120
QY 121 TGCCCGACACTGAGACGCTGTTCCAGCGTCAAAAGAGAGACTGCGCGCGGCAACCCGG 180
DB 121 TGCCCGACACTGAGACGCTGTTCCAGCGTCAAAAGAGAGACTGCGCGCGGCAACCCGG 180
QY 181 GAGAGGAGGAGGCAAGAAAGAAACGGAATTCGGTCTTGGGCCAGGTCTTTTGACC 240
DB 181 GAGAGGAGGAGGCAAGAAAGAAACGGAATTCGGTCTTGGGCCAGGTCTTTTGACC 240
QY 241 AGAGTTTTTCCATGTGGACGCTCTTCAATGAGAGTGTCCCGGTGCTTTAGACGGA 300
DB 241 AGAGTTTTTCCATGTGGACGCTCTTCAATGAGAGTGTCCCGGTGCTTTAGACGGA 300
QY 301 CTGCGGTCTCTAAAGGTTCGACCATGTGTGGCGCGGACCCGCTGTCTTCTAGCGTTGCTGC 360
DB 301 CTGCGGTCTCTAAAGGTTCGACCATGTGTGGCGCGGACCCGCTGTCTTCTAGCGTTGCTGC 360
QY 361 TTCCCCAGGTCTCTCTGGCGCGCGCTGCGCTTCCGAGCTGCGGCGCAGGAAGT 420
DB 361 TTCCCCAGGTCTCTCTGGCGCGCGCTGCGCTTCCGAGCTGCGGCGCAGGAAGT 420
QY 421 TCGCGCGCGGTCTGTCGGCGCGCCCTCATCTCCAGCCCTCTGACGAGTCTCTGAGCGGAGT 480
DB 421 TCGCGCGCGGTCTGTCGGCGCGCCCTCATCTCCAGCCCTCTGACGAGTCTCTGAGCGGAGT 480
QY 481 TCGAGTTGCGGTCTGTCAGCATGTTCCGCTGAAACAGAGACCCACCCAGCAGGAGC 540
DB 481 TCGAGTTGCGGTCTGTCAGCATGTTCCGCTGAAACAGAGACCCACCCAGCAGGAGC 540
QY 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGAGGCACTCAGGTCAAGCGGCTCAC 600
DB 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCGAGGCACTCAGGTCAAGCGGCTCAC 600
QY 601 CGCGCCCAAGACACCGGTTGGAGAGGGCAGCCAGCGGAGCCAACTGTGGCAGCTTCC 660
DB 601 CGCGCCCAAGACACCGGTTGGAGAGGGCAGCCAGCGGAGCCAACTGTGGCAGCTTCC 660
QY 661 ACCATGAAGAATCTTTTGAAGAACTTACAGAAACAGAGTGGGAAACAAACCGGAGATTCT 720
DB 661 ACCATGAAGAATCTTTTGAAGAACTTACAGAAACAGAGTGGGAAACAAACCGGAGATTCT 720
QY 721 TCTTTAAATTTAAGTTCTATCCCAAGGAGGAGTTTATCACCCTCAGCAGAGCTTCAGGTTT 780

Db 721 TCTTTAATTTAAGTTCTATCCACGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTTCATCACCGAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTTCATCACCGAATTAATA 840
Qy 841 TTTATGAATCATATAAACTCTCAACAGCCAACTCGAAATTCCTCCGTCAGCAGACTTTTGG 900
Db 841 TTTATGAATCATATAAACTCTCAACAGCCAACTCGAAATTCCTCCGTCAGCAGACTTTTGG 900
Qy 901 ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 960
Db 901 ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 960
Qy 961 TGATCGGTGACATGCAAGGACACGCAACATGGAATTCGTTGGTGAAGTGGCCCACT 1020
Db 961 TGATCGGTGACATGCAAGGACACGCAACATGGAATTCGTTGGTGAAGTGGCCCACT 1020
Qy 1021 TGGAGGAGAAACAAGTGTCTCCAAAGAGACATGTTAGGATAGCAGGTCTTTTGACCAAG 1080
Db 1021 TGGAGGAGAAACAAGTGTCTCCAAAGAGACATGTTAGGATAGCAGGTCTTTTGACCAAG 1080
Qy 1081 ATGAACACAGCTGGTCAAGATAAGGCCATTTGCTAGTAACCTTTTGGCCATGATGCAAAAG 1140
Db 1081 ATGAACACAGCTGGTCAAGATAAGGCCATTTGCTAGTAACCTTTTGGCCATGATGCAAAAG 1140
Qy 1141 GGCATCTCTCCAAAGAGAAACCGTCAAGCCAAACACACAGCGGAAACGCTCTTA 1200
Db 1141 GGCATCTCTCCAAAGAGAAACCGTCAAGCCAAACACACAGCGGAAACGCTCTTA 1200
Qy 1201 AGTCAGCTGTAAGAGACACCTTTGTACGTGGACTTCAGTACGTGGGTGGGAATGACT 1260
Db 1201 AGTCAGCTGTAAGAGACACCTTTGTACGTGGACTTCAGTACGTGGGTGGGAATGACT 1260
Qy 1261 GGAATGTGGTCTCCCGGGTATCAAGCTTTTACTGCGAGAGAAATGCCCTTTTCTCTC 1320
Db 1261 GGAATGTGGTCTCCCGGGTATCAAGCTTTTACTGCGAGAGAAATGCCCTTTTCTCTC 1320
Qy 1321 TGGCTGATCATCTGAACCTCACTAATCATGATGATGTTTTCAGACGTTGGTCAACTCTCTTA 1380
Db 1321 TGGCTGATCATCTGAACCTCACTAATCATGATGATGTTTTCAGACGTTGGTCAACTCTCTTA 1380
Qy 1381 ACTCTAGATCTCTAAGCATGCTGTGTCGCGACAGAACTCAGTGTCTCGATGCTGT 1440
Db 1381 ACTCTAGATCTCTAAGCATGCTGTGTCGCGACAGAACTCAGTGTCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGAAATGAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGGTT 1500
Qy 1501 GTGGGTGTCGTAGTACAGCAAAATTAATACATAAATATATATATA 1547
Db 1501 GTGGGTGTCGTAGTACAGCAAAATTAATACATAAATATATATATA 1547

RESULT 12

US-10-917-265-1
; Sequence 1, Application US/10917265
; Publication No. US20050136042A1
; GENERAL INFORMATION:
; APPLICANT: BETZ, OLIVER B.
; APPLICANT: BETZ, VOLKER M.
; APPLICANT: EVANS, CHRISTOPHER H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TISSUE REPAIR
; FILE REFERENCE: BMW-004.01
; CURRENT APPLICATION NUMBER: US/10/917,265
; CURRENT FILING DATE: 2004-08-11
; PRIOR APPLICATION NUMBER: 60/494,484
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1547

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-917-265-1
Query Match 100.0%; Score 1547; DB 9; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTGAACTTGCAGGAGAAATACTTGCACACCCCACTTTTGGCCGGTGCCTT 60
Db 1 GGGGACTTCTTGAACTTGCAGGAGAAATACTTGCACACCCCACTTTTGGCCGGTGCCTT 60
Qy 61 TGCCCCAGCGGAGCTGCTTCCGATCTCCGAGCCCAACCGCCCTCCACTTCTCCGCT 120
Db 61 TGCCCCAGCGGAGCTGCTTCCGATCTCCGAGCCCAACCGCCCTCCACTTCTCCGCT 120
Qy 121 TGCCCCAGCACATGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGCGCGGCAACCGG 180
Db 121 TGCCCCAGCACATGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGCGCGGCAACCGG 180
Qy 181 GAGAGGAGGAGGCAAGAAAGAGACGACATTCGGTCTTTCGCGCAGGTCTCTTGAAC 240
Db 181 GAGAGGAGGAGGCAAGAAAGAGACGACATTCGGTCTTTCGCGCAGGTCTCTTGAAC 240
Qy 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGAGACGTGTCTCCCGCTGCTCTTTAGACGA 300
Db 241 AGAGTTTTTCCATGTGACGCTCTTTCAATGAGACGTGTCTCCCGCTGCTCTTTAGACGA 300
Qy 301 CTGCGGTCTCTTAAAGTCCGACCATGCTGGCGCGGACCCCGCTGTCTTCTAGCGTTGCTGC 360
Db 301 CTGCGGTCTCTTAAAGTCCGACCATGCTGGCGCGGACCCCGCTGTCTTCTAGCGTTGCTGC 360
Qy 361 TTCCCGAGGTCTCTTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 TTCCCGAGGTCTCTTGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 421 TCGCGGCGGCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 TCGCGGCGGCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 481 TCGAGTTTGGCGGTCTCAGCATGTTCCGCTTGAAGACAGAGACCCACCCAGCAGGAGCG 540
Db 481 TCGAGTTTGGCGGTCTCAGCATGTTCCGCTTGAAGACAGAGACCCACCCAGCAGGAGCG 540
Qy 541 CGGTGTCGCCCTTACATGCTAGACCTGTATGCGAGGCACTCAGGTGAGCGGGCTCAC 600
Db 541 CGGTGTCGCCCTTACATGCTAGACCTGTATGCGAGGCACTCAGGTGAGCGGGCTCAC 600
Qy 601 CCGCCCCAGACCCCGGTTGAGAGGGCAGCCAGCGGACCAACACCTGTCGCGAGCTTCC 660
Db 601 CCGCCCCAGACCCCGGTTGAGAGGGCAGCCAGCGGACCAACACCTGTCGCGAGCTTCC 660
Qy 661 ACCATGAAGAACTTTTGGAAAGAACTTACAGAAACGAGTGGGAAAAACAAACCGGAGATTCT 720
Db 661 ACCATGAAGAACTTTTGGAAAGAACTTACAGAAACGAGTGGGAAAAACAAACCGGAGATTCT 720
Qy 721 TCTTTAATTTAAGTTCTATCCCAAGGAGTTTATCCTCAGCAGAGCTTCAGGTTT 780
Db 721 TCTTTAATTTAAGTTCTATCCCAAGGAGTTTATCCTCAGCAGAGCTTCAGGTTT 780
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTTCATCACCGAATTAATA 840
Db 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTTCATCACCGAATTAATA 840
Qy 841 TTTATGAATCATATAAACTCTCAACAGCCAACTCGAAATTCCTCCGTCAGCAGACTTTTGG 900
Db 841 TTTATGAATCATATAAACTCTCAACAGCCAACTCGAAATTCCTCCGTCAGCAGACTTTTGG 900
Qy 901 ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 960
Db 901 ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTTCATGTCAACCCCGCTG 960
Qy 961 TGATCGGTGACATGCAAGGACACGCAACATGGAATTCGTTGGTGAAGTGGCCCACT 1020
Db 961 TGATCGGTGACATGCAAGGACACGCAACATGGAATTCGTTGGTGAAGTGGCCCACT 1020

Db 1201 AGTCAGCTGTAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGTGGAACTACT 1260
Qy 1261 GGATTGTGGCTCCCGGGGTATCAGCGCTTTTACTGCGCAGGAGAAATGCCCTTTTCCCTC 1320
Db 1261 GGATTGTGGCTCCCGGGGTATCAGCGCTTTTACTGCGCAGGAGAAATGCCCTTTTCCCTC 1320
Qy 1321 TGGCTGATCATCTGAATCCCACTAATCATGCGCATTTGTTTCAGACGTTGCTCAACTCTGTTA 1380
Db 1321 TGGCTGATCATCTGAATCCCACTAATCATGCGCATTTGTTTCAGACGTTGCTCAACTCTGTTA 1380
Qy 1381 ACTCTAAGATTCTTAAGSCATGCTGTGTCGCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Db 1381 ACTCTAAGATTCTTAAGSCATGCTGTGTCGCGACAGAACTCAGTGTCTATCTCGATGCTGT 1440
Qy 1441 ACCTTGACGAGAAATGAAGTTGTATTAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Db 1441 ACCTTGACGAGAAATGAAGTTGTATTAAGAACTATCAGGACATGTTGTGAGGGTT 1500
Qy 1501 GTGGGTGTCGTAGTACAGCAAAATTAATACATATAATATATATA 1547
Db 1501 GTGGGTGTCGTAGTACAGCAAAATTAATACATATAATATATATA 1547

RESULT 14

US-09-804-625-3
; Sequence 3, Application US/09804625
; Publication No. US20030049826A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; Rosen, Vicki A.
; Wozney, John M.
; TITLE OF INVENTION: No. US20030049826A1el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/804,625
; FILING DATE: 09-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/925,779
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: 5160C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; CELL TYPE: Osteosarcoma Cell Line
; CELL LINE: U-2OS

IMMEDIATE SOURCE:
LIBRARY: U2OS cDNA in Lambda GT10
CLONE: Lambda U2OS-39
POSITION IN GENOME:
UNITS: bp
FEATURE:
NAME/KEY: CDS
LOCATION: 356..1546
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1202..1543
FEATURE:
NAME/KEY: mRNA
LOCATION: 14..1607
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 356..424
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-804-625-3
Query Match 100.0%; Score 1547; DB 3; Length 1607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGACTTCTTTGAACCTTGACAGGAGAAATACTTGGCACCACCCCACTTTTGGCCCGGTGCTT 60
Db 33 GGGGACTTCTTTGAACCTTGACAGGAGAAATACTTGGCACCACCCCACTTTTGGCCCGGTGCTT 92
Qy 61 TGCCCCCAGCGGAGCTGCTTTCGCCATCTCCGAGCCCCCACCAGCCCTTCACTTCTCGGCCT 120
Db 93 TGCCCCCAGCGGAGCTGCTTTCGCCATCTCCGAGCCCCCACCAGCCCTTCACTTCTCGGCCT 152
Qy 121 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGGCGCGGACCCGG 180
Db 153 TGCCCCGACACTGAGACGCTGTTCCAGCGTGAAGAGAGACTGCGGCGCGGACCCGG 212
Qy 181 GAGAGGAGGAGGCAAGAAAGAGACGACATTCGTCCTTCGCGCAGAGTCTCTTTCAGCC 240
Db 213 GAGAGGAGGAGGCAAGAAAGAGACGACATTCGTCCTTCGCGCAGAGTCTCTTTCAGCC 272
Qy 241 AGAGTTTTTTCATGTGGACGCTCTTTTCAATGGACGTTGCCCGCGTCTTCTTAGACGA 300
Db 273 AGAGTTTTTTCATGTGGACGCTCTTTTCAATGGACGTTGCCCGCGTCTTCTTAGACGA 332
Qy 301 CTGCGGTCTCTTAAAGTTCAGACCATGCTGCGCGGAGCCCGCTCTCTTACGCTTGTGTC 360
Db 333 CTGCGGTCTCTTAAAGTTCAGACCATGCTGCGCGGAGCCCGCTCTCTTACGCTTGTGTC 392
Qy 361 TTCCCCAGGTCTCTTCTGCGGCGCGGCTGCGCTTCGTCGAGCTGGCGCGCAGGAAGT 420
Db 393 TTCCCCAGGTCTCTTCTGCGGCGCGGCTGCGCTTCGTCGAGCTGGCGCGCAGGAAGT 452
Qy 421 TCGCGCGCGGTCTCTGCGGCGCGGCTCTTCCAGCCCTCATCCAGCCCTCTGAGCGAGT 480
Db 453 TCGCGCGCGGTCTCTGCGGCGCGGCTCTTCCAGCCCTCATCCAGCCCTCTGAGCGAGT 512
Qy 481 TCGAGTTGCGGCTGCTCAGCATGTTGGCCCTGAAAAGAGACCCACCCAGCAGGAGACG 540
Db 513 TCGAGTTGCGGCTGCTCAGCATGTTGGCCCTGAAAAGAGACCCACCCAGCAGGAGACG 572
Qy 541 CCGTGGTGGCCCCCTACATGCTAGACCTGTATCGCAGGCACTCAGGTTCAGCGGCTCAC 600
Db 573 CCGTGGTGGCCCCCTACATGCTAGACCTGTATCGCAGGCACTCAGGTTCAGCGGCTCAC 632
Qy 601 CCGCCCCAGACCCAGGTTCGAGAGGCGCAGCCAGCCAGCAACACACTGTGGCAGCTTCC 660
Db 633 CCGCCCCAGACCCAGGTTCGAGAGGCGCAGCCAGCCAGCAACACACTGTGGCAGCTTCC 692
Qy 661 ACCATGAGAAATCTTTGGAAGAACTACACAGAAAGAGTGGGAACAAACCCGGAGATTCT 720
Db 693 ACCATGAGAAATCTTTGGAAGAACTACACAGAAAGAGTGGGAACAAACCCGGAGATTCT 752
Qy 721 TCTTTAATTTAAGTTTCTATCCCCAGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTT 780

Db 273 AGAGTTTTCATGTGGAGCTCTTTCAATGGAAGTGTCCCGGCTGCTTTTAGACGA 332
Qy 301 CTGGGCTCTCTAAAGTTCGACCAATGATGGGCGGGAACCCGCTGTCTTCTAGCGTGTGTC 360
Db 333 CTGGGCTCTCTAAAGTTCGACCAATGATGGGCGGGAACCCGCTGTCTTCTAGCGTGTGTC 392
Qy 361 TTCCCGGAGTCTCTTGGGCGGCGGCTGGCTGCTTCCGAGCTGGGCGGAGGAGT 420
Db 393 TTCCCGGAGTCTCTTGGGCGGCGGCTGGCTGCTTCCGAGCTGGGCGGAGGAGT 452
Qy 421 TCGGCGGCGCTCTGTCGGGCGGCGGCTCTCATCCAGCCCTCTGAGAGGCTCTGAGCGAGT 480
Db 453 TCGGCGGCGCTCTGTCGGGCGGCGGCTGGCTGCTTCCGAGCTGGGCGGAGGAGT 512
Qy 481 TCGAGTTGCGGCTCTGTCAGATGTTTCGCGCTGAAACAGAGACCCACCCAGCAGGAGC 540
Db 513 TCGAGTTGCGGCTCTGTCAGATGTTTCGCGCTGAAACAGAGACCCACCCAGCAGGAGC 572
Qy 541 CCGTGGTCCCGCTTACATGCTAGACCTGTATCCGAGCACTCAGGTCAGCGCGGCTCAC 600
Db 573 CCGTGGTCCCGCTTACATGCTAGACCTGTATCCGAGCACTCAGGTCAGCGCGGCTCAC 632
Qy 601 CCGCGCCAGACCAACCGGTTGGAGAGGCGAGCCAGCCAGCCAACTGTGCGCAGCTTCC 660
Db 633 CCGCGCCAGACCAACCGGTTGGAGAGGCGAGCCAGCCAGCCAACTGTGCGCAGCTTCC 692
Qy 661 ACCATGAAGAATCTTTTGAAGAACTTACAGAAACGAGTGGGAAACAAACCCGAGATCT 720
Db 693 ACCATGAAGAATCTTTTGAAGAACTTACAGAAACGAGTGGGAAACAAACCCGAGATCT 752
Qy 721 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 780
Db 753 TCTTTAATTTAAGTTCTATCCCGAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTT 812
Qy 781 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCAGAAATTAATA 840
Db 813 TCCGAGAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCAGAAATTAATA 872
Qy 841 TTTATGAATAATCAATAAACCTGCAACAGCCAACTCGAAATCCCGGTGACCAAGCTTTTGG 900
Db 873 TTTATGAATAATCAATAAACCTGCAACAGCCAACTCGAAATCCCGGTGACCAAGCTTTTGG 932
Qy 901 ACACAGGTTGGTGAATCAGAAATGCAAGAGTGGGAAAGTTTGTATGTCACCCCGCTG 960
Db 933 ACACAGGTTGGTGAATCAGAAATGCAAGAGTGGGAAAGTTTGTATGTCACCCCGCTG 992
Qy 961 TGATGCGGTGACTGCAACGGGACACGCCAACCATGGATTCGTGTTGGAAGTGGCCCACT 1020
Db 993 TGATGCGGTGACTGCAACGGGACACGCCAACCATGGATTCGTGTTGGAAGTGGCCCACT 1052
Qy 1021 TGGAGGAGAAACAAAGTGTCTCCAAAGAGACATGTTAGGATAAGCAGGCTTTTGACCAAG 1080
Db 1053 TGGAGGAGAAACAAAGTGTCTCCAAAGAGACATGTTAGGATAAGCAGGCTTTTGACCAAG 1112
Qy 1081 ATGACACAGCTGGTCAAGATAGGCAATTTGTAGTAACTTTTGGCCATGATGGAAG 1140
Db 1113 ATGACACAGCTGGTCAAGATAGGCAATTTGTAGTAACTTTTGGCCATGATGGAAG 1172
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Db 1173 GGCAATCTCTCCAAAAAGAGAAAAAGTCAAGCCAAACACAAAAACAGCGGAAACGCCCTTA 1232
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Db 1293 GGATTTGGCTCCCCCGGGTATCAGCCCTTTTACTGCGAGAGATGCCCTTTTCTC 1352
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Db 1473 ACCTTGACGAGAATGAAAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGTTT 1532
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Search completed: January 10, 2006, 23:43:18
Job time : 929 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1547	100.0	1547	6	US-10-650-326B-10	Sequence 10, Appl
2	1227.2	79.3	1260	7	US-11-051-568-4	Sequence 4, Appli
3	1032.2	66.7	2738	7	US-11-136-527-2371	Sequence 2371, Ap
4	345	24.2	1751	6	US-10-650-326B-11	Sequence 11, Appl
5	375	24.2	1788	7	US-11-051-568-6	Sequence 6, Appli
6	372.2	24.1	1586	7	US-11-051-568-18	Sequence 6, Appli
7	371.4	24.0	1900	7	US-11-136-527-2142	Sequence 18, Appl
8	201	13.0	600	7	US-11-136-527-6238	Sequence 2142, Ap
9	192.8	12.5	525	7	US-11-051-568-16	Sequence 16, Appl
10	159.6	10.3	1400	7	US-11-136-527-6467	Sequence 16, Appl
11	124.4	8.0	405	6	US-10-816-768-90	Sequence 90, Appl
12	123.6	8.0	1252	6	US-10-131-826A-341	Sequence 341, Appl
13	122	7.9	1212	9	US-11-091-334-1	Sequence 1, Appli
14	122	7.9	1764	7	US-11-136-527-3392	Sequence 3392, Ap
15	119	7.7	314	7	US-11-051-568-33	Sequence 33, Appl
16	118	7.6	1004	7	US-11-051-568-10	Sequence 10, Appl
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18	118	7.6	1505	7	US-11-051-568-12	Sequence 12, Appl
19	118	7.6	1822	6	US-10-816-768-38	Sequence 38, Appl
20	118	7.6	1822	6	US-10-650-326B-17	Sequence 17, Appl
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RESULT 2
US-11-051-568-4
: Sequence 4, Application US/11051568
: Publication No. US20050255141A1
: GENERAL INFORMATION:
: APPLICANT: OPPERMAN, HERMANN
: OZKAYNAK, ENGIN
: KUBERASAMPATH, THANGAVEL
: RUEGER, DAVID C.
: PANG, ROY H.L.
: TITLE OF INVENTION: OSTEOGENIC DEVICES
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TESTA, HURWITZ & THIBEAULT
: STREET: 125 HIGH STREET
: CITY: BOSTON
: STATE: MASSACHUSETTS
: COUNTRY: U.S.A.
: ZIP: 02110
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/11/051,568
: FILING DATE: 04-Feb-2005
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 10/321,799
: FILING DATE: 17-DEC-2002
: APPLICATION NUMBER: US 09/148,925
: FILING DATE: 8-SEP-1998
: APPLICATION NUMBER: US 08/449,699
: FILING DATE: 24-MAY-1995
: APPLICATION NUMBER: US 08/147,023
: FILING DATE: 1-NOV-1993
: APPLICATION NUMBER: US 07/841,646
: FILING DATE: 21-FEB-1992
: APPLICATION NUMBER: US 07/827,052
: FILING DATE: 28-JAN-1992
: APPLICATION NUMBER: US 07/579,865
: FILING DATE: 7-SEP-1990
: APPLICATION NUMBER: US 07/621,849
: FILING DATE: 4-DEC-1990
: APPLICATION NUMBER: US 07/621,988
: FILING DATE: 4-DEC-1990
: APPLICATION NUMBER: US 07/810,560
: FILING DATE: 20-DEC-1991
: APPLICATION NUMBER: US 07/569,920
: FILING DATE: 20-AUG-1990
: APPLICATION NUMBER: US 07/600,024
: FILING DATE: 18-OCT-1990
: APPLICATION NUMBER: US 07/599,543
: FILING DATE: 18-OCT-1990
: APPLICATION NUMBER: US 07/616,374
: FILING DATE: 21-NOV-1990
: APPLICATION NUMBER: US 07/483,913
: FILING DATE: 22-FEB-1990
: APPLICATION NUMBER: US 07/179,406
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FILING DATE: 08-APR-1988
APPLICATION NUMBER: US 07/232,630
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 07/315,342
FILING DATE: 23-FEB-1989
APPLICATION NUMBER: US 07/660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,613
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,623
FILING DATE: 17-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: CDS
LOCATION: 9..1196
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "CBMP2A"
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-051-568-4

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB	181	TCAGATGTTGGCTGGAACAGAGACCCACCCCGAGGAGCGCGCTGGTGGCCCGCT	240
QY	556	ACATGCTAGACCTGTATCGAGGCACTCAGTTCAGCGGGCTCACCCCGCCCGAGACCC	615
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QY	616	GTTTGGAGGGGAGCGAGCGGAGCAACACTGTGCGCAGCTTCCACCATTGAAGAATCTT	675
DB	301	GTTTGGAGGGGAGCGAGCGGAGCAACACTGTGCGCAGCTTCCACCATTGAAGAATCTT	360
QY	676	TGGAAGAACTACAGAAAGAGTGGGAAACAAACCGGAGATCTCTTTTAATTAAGTT	735
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DB	421	CTATCCCGAGGAGGAGTTTATACCTTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGC	480
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DB	661	CACAGGACAGCCCAACCATGGAATTCGTGGTGGAGTGGCCCACTTTCAGGAGGAAACAAG	720
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DB	721	GTGTCTCCAGAGACATGTTAGGATAAGCAGGTTCTTTCACCAAGATGAACACAGCTGGT	780
QY	1096	CACAGATAAGGCCATTGTCTAGTAACTTTTGGCCATGATGGAAGGCGATCTCTCCACA	1155
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DB	961	CGGGGTATCACGCCCTTTTACTGCCACGAGAAATGCCCTTTCTCTGGCTGATCATCTGA	1020
QY	1336	ACTCCATTAATCATGCCATTTGTTCCAGAGTTGGTTCNACTCTGTTAACTTAAGATTCTTA	1395
DB	1021	ACTCCATTAATCATGCCATTTGTTCCAGAGTTGGTTCNACTCTGTTAACTTAAGATTCTTA	1080
QY	1396	AGGCATGCTGTGTCGCCGACAGAACTCAGTCTATCTCGATGCTGTACCTTGACGAGAAATG	1455
DB	1081	AGGCATGCTGTGTCGCCGACAGAACTCAGTCTATCTCGATGCTGTACCTTGACGAGAAATG	1140
QY	1456	AAAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTGTCGCTAGT	1515
DB	1141	AAAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTGTCGCTAGT	1200
QY	1516	ACAGCAAAATTAATACATAAATATATATATA 1547	
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US-11-136-527-2371
; Sequence 2371, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2371
; LENGTH: 2738

REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STX-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURE:
NAME/KEY: CDS
LOCATION: 403..1626
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "CBMP2B"
/evidence= EXPERIMENTAL
/note= "CBMP2B (CDNA)"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-11-051-568-6
Query Match 24.2%; Score 375; DB 7; Length 1788;
Best Local Similarity 61.0%; Pred. No. 5.7e-98;
Matches 672; Conservative 0; Mismatches 405; Indels 24; Gaps 3;
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QY 614 CCGGTG- - - - -GAGAGGGAGCGCAGCGGAGCCAACTGTGCGCAGCTTCCACC 663
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DB 767 ACAGAAACATCTGGAGAACTCCAGGAGCAAGTGAATCTGTCTTCTGTTCTCTCT 826
QY 724 TTAATTTAAGTTCTATCCCGCAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTTTC 783
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RESULT 6
US-11-051-568-18
; Sequence 18, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; OZKANAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568
; FILING DATE: 04-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/321,799
; FILING DATE: 17-DEC-2002
; APPLICATION NUMBER: US 09/148,925
; FILING DATE: 8-SEP-1998
; APPLICATION NUMBER: US 08/449,699
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 1-NOV-1993

APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/827,052
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: US 07/579,865
FILING DATE: 7-SEP-1990
APPLICATION NUMBER: US 07/621,849
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/621,988
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/810,560
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 07/569,920
FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 07/600,024
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/599,543
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/616,374
FILING DATE: 21-NOV-1990
APPLICATION NUMBER: US 07/483,913
FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
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APPLICATION NUMBER: US 07/232,630
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APPLICATION NUMBER: US 07/315,342
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APPLICATION NUMBER: US 07/660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,613
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,623
FILING DATE: 17-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1586 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1257
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "CBMP2B-2"
/note= "CBMP2B-2 - FUSION"
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Query Match 24.1%; Score 372.2; DB 7; Length 1586;
Best Local Similarity 61.4%; Pred. No. 3.5e-97;
Matches 662; Conservative 0; Mismatches 393; Indels 24; Gaps 3;
QY 458 CTCTGACGAGCTCTGAGCGAGTTCGAGTTGGCGGTGCTCAGCATGTTCCGGCTCGAAACA 517
Db 180 CCGGGAGAGCTCTCTCGGGAGCTTCGAGGCGACATCTCTGCGAGATGTTGGGCTGGCGG 239
QY 518 GAGACCCACCCAGCAGGAGCGCGGTGTCGCCCTCATGCTAGACCTCTATCGCAG 577
Db 240 CCGCCGCGAGCTAGCAAGAGTGGCGTCACTCCGGAGCTACATGCGGATCTTTACCGGCT 299

QY 578 GCACCTCAGGTCTAGCGG--GGCTCACCCGCGCCCGCAGACCAACCGGTTG-----GAGAG 625
Db 300 TCAGTCTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 359
QY 626 GCGAGCCAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 685
Db 360 CCGGCGAGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 419
QY 686 ACCGAGAAACGAGTGGGAGAAACAAACCGGAGATTTCTTTTAAATTTAAATTTAAATTTAA 745
Db 420 CCGGAGACAGTGAATACTCTGCTTTTCTTTTAACTCTGAGGAGGAGGAGGAGGAGGAGGAG 479
QY 746 GCGAGGAGTTTATCACCTCAGCAGAGCTTTTCCGAGAAACAGATGCAAGATGCTTTT 805
Db 480 GAAACGAGCGGATCTCTCTGAGAGCTTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 539
QY 806 AGGAGAAACATAGCAGTTTCCATCAGGATTTAATTTATGAAATCATAAATCATAAATCAG 865
Db 540 TGATTTGGGAAAGGGGCTTTCCACCGTATAAATTTATGAGGTTATGAAAGCCCCCAGCAGA 599
QY 866 AGCCAACTCGAAATTTCCCGGTGACGAGCTTTTGGACACCAAGTTGGTGAATCAGAATGC 925
Db 600 AGTGTGCTCGGCGACCTCATCAGAGCTACTGACACAGAGCTGCTGACCAACCAATGT 659
QY 926 AAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTGTGATGCGGTGGAGTGCACAGGAGCA 985
Db 660 GACAGGTGGGAAACTTTTGTATGTGAGCGCTTCCGCTGCGTGGACCGGAGAGCA 719
QY 986 CGCCAAACATGAGTTTGGTGGAGAGTGGCCCATTTGGAGGAGAGAAACAGAGTGTCTCCAA 1045
Db 720 GCCAACTATGGGCTAGCCATTTGAGGTGACTCACCTCCATCAGACTCGGACCCACAGGG 779
QY 1046 GAGACATCTTAGGATAAGCAGGTCTTTGCCAACAAGATGAAACACAGCTGTCTCAGATAG 1105
Db 780 CAGCATGTCTAGGATTTAGCGGATTTACCTCAAGGGAGTGGGAATTTGGGCCAGCTCCG 839
QY 1106 GCCATTGTCTAGTAACCTTTTGGCCATGATGGAAGGGGATCTCTCCCAAAAAGAGAAAA 1165
Db 840 GCCCTCTCTGTACCTTTTGGCCATGATGCGCGGGGCCATGCTTGACCCGACGCGGAG 899
QY 1166 AGCTCAAGCCAAAACAACAGCGGAGAAACGCGCTT-----AAGTCCAGCTGTAA 1213
Db 900 GCGCAAGCGGTAGCCCTAAGCATCACTCAGCGGGGCCAGGAGAGAAATAAGAACTGCGG 959
QY 1214 GAGACACCTTTGTACGTGGACTTCAGTGCAGTGGGGTGGATGATGATGATGATGATGATG 1273
Db 960 GCGCCACTCGCTCTATGTGGACTTCAGCGATGTGGGGTGGAAATGATGATGATGATGATG 1019
QY 1274 CCGGGGTATCAGCGCTTTTACTGCGCAGGAGAAATGCCCTTTTCTCTGCTGATCATCT 1333
Db 1020 ACCAGGCTACGAGGCTTCTACTGCGATGGGAGCTGCCCTTTCCACTGGCTGACCACT 1079
QY 1334 GAATCCACTAATCATGCAATTTTTCAGAGCTTGTGTCAGCTCTGTGTAATCTTAAGATTCC 1393
Db 1080 CAACTCAACCAACCATGCAATTTGTCAGACCCCTGCTCAATTTCTCAATTTCCAGTATCC 1139
QY 1394 TAAGCATGCTGTGTCGCGACAGACTCAGTGCATCTCGATGCTGTGCTGCTGCTGAGGAA 1453
Db 1140 CAAAGCCTGTTGTGTCGCGACCTGAATCTGAGTGCCTCTCCATGCTGTACTCTGATGAT 1199
QY 1454 TGAAGAGGTGTATTAAAGAACTATCAGGACATGTTGTGGAGGGTGTGGGTGTGCT 1512
Db 1200 TGATAGGTGTACTGAGAAATTTATCAGGAGATGTTAGAGGAGTGTGGGTGTGCT 1258

RESULT 7

US-11-136-527-2142
; Sequence 2142, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

```
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2142
; LENGTH: 1900
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2142

Query Match      24.0%; Score 371.4; DB 7; Length 1900;
Best Local Similarity 60.5%; Pred. No. 6.5e-97;
Matches 666; Conservative 5; Mismatches 406; Indels 24; Gaps 3;

Qy 436 CGGGCGCCCTCATCCAGCCCTCTGACAGGTCCTGAGCGAGTTCAGTGTGGGTGC 495
Db      |||||
Qy 525 CGGAGGAGCGGCTCAGGCGAGGCCATGAGCTCTCGGGACTTCGAGGCGACATTC 584
Db      |||||
Qy 496 TCAGATGTTGGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGTGCCCCCT 555
Db      |||||
Qy 585 TGCAGATGTTGGGCTGCGCGCGCTCGCAGCCGAGCAAGAGCGCGCTCATCCGGATT 644
Db      |||||
Qy 556 ACATGCTAGACTGTATCGCAGGCACTCAGTTCAGCGCGGCTCACCCGCCAGCACCC 615
Db      |||||
Qy 645 ACATGAGGAGCTTTACCGGCTCCAGTCTGGGAGGAGGAGGAGAGAGAGAGCAGG 704
Db      |||||
Qy 616 GGTG-----GAGAGGGCAGCCAGCCAGCCAGCAACACTGTGCGAGCTTCC 660
Db      |||||
Qy 705 GAACCGGCTTGAGTACCTGAGSGTCTGCCAGCAGAGCCAACTGTGAGGAGTTCC 764
Db      |||||
Qy 661 ACCATGAAGAATCTTTGAAGAACTACAGAAACGAGTGGGAAACAAACCCGAGATTCT 720
Db      |||||
Qy 765 ATCAGAGAACATCTTGAGAACATCCAGGAGCAGTGGAGAGCTCTGCTTTTGGTTCT 824
Db      |||||
Qy 721 TCTTTAATTAAGTCTATCCCAACGAGGAGTTTATCACCTCAGCAGAGCTTCAGTTT 780
Db      |||||
Qy 825 TCTTTAACCCTCAGCAGCATCCAGAGATAGGAGTATCTCTCGAGAGCTCGGGTAT 884
Db      |||||
Qy 781 TCCGAGAACAGATGCAAGATCTTTAGGAAACAAATAGCAGTTTCCATCACCGAATTATA 840
Db      |||||
Qy 885 TTCGGAGCAGGTGGACCCAGGCGCTGACTGGGACAGGGCTTCCACCGTATTAACATT 944
Db      |||||
Qy 841 TTTATGAATCATAAACCTGCAACAGCCAACTCGAAATTCCTCCGTCGACACACTTTGG 900
Db      |||||
Qy 945 ATGAGGTATGAAGCCCCCAGCAGAAATGTTGCTGACACCTCATCACAGCACTACTGG 1004
Db      |||||
Qy 901 ACACGAGTTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTGTGATGTCAACCCCGTG 960
Db      |||||
Qy 1005 ACACAGACTAGTCCRTCAATGTGACACGGTGGGAAACTTTGATGTGAGCCCTGAG 1064
Db      |||||
Qy 961 TGATGCGGTGACTGCAACAGGACACGCCAACCATGAGTTGTTGGTGAAGTGCCCACT 1020
Db      |||||
Qy 1065 TCCTTCGATGACCCGGGAAAGCAACCAACTATGGCTGGCCATGAGGTGACTACC 1124
Db      |||||
Qy 1021 TGGAGGAGAAACAAAGGTGTCTCCAAGAGACATGTTAGGATAAGCAGTCTTTGACCAAG 1080
Db      |||||
Qy 1125 TCCACAGACACGAGCCCAACAGGCGCCAAATGTCAAGATTAGCCGATCGTTACTCAAG 1184
Db      |||||
Qy 1081 ATGAACACAGCTGTCACAGATAGGCCATTTGCTAGTAACTTTTGGCCATGATGGAAG 1140
Db      |||||
Qy 1185 GGAATGGAAATGGGCGCCAACTCCGGCCCCCTCTGGTCAATTTTGGCCACATGGCCGG 1244
Db      |||||
Qy 1141 GGCATCTCTCT---CCACAAAAGAGAAACCTCAAGCCAAACACAAACAGCGGAAACGCC 1197
Db      |||||
Qy 1245 GTCATACCTTGACCGCGAGGAGCCAGCGTAGTCCCAAGCATCAACCCAGCGCTCCA 1304
Db      |||||
Qy 1198 TTAAGTCAG-----CTGTAAGAGACACCTTTGTTAGCTGGACTTCAGTGAOCTGGGT 1251
Db      |||||
Qy 1305 GGAAGAGAAATAGAACTGCGCGTCCGCTTACGCTGAGCTTCAGTGAOCTGGGCT 1364
Db      |||||
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Qy 1252 GGAATGACTGATGTGGCTCCCGGGGTATCACGCTTTTACTGCAACGAGAAATGCC 1311
Db      |||||
Qy 1365 GGAATGATTTGATGCTGGCCCGCCWCCAGGCTTACCAGGCTTCTACTGCCACGGGACTGTC 1424
Db      |||||
Qy 1312 CTTTTCCTCTGGCTGATCATCTGAATCTCCACTAAATCAAGCAATTTGTTCAGACGTTGGTCA 1371
Db      |||||
Qy 1425 CTTTTCACCTGGCGGCCACCTCAACTCAACCAATCATGCCATTTGTGCAGACCCCTGGTCA 1484
Db      |||||
Qy 1372 ACTCTGTTAACTCTAAGATTTCTTAAGGCATGCTGTGTCGCCGACAGAACTCAGTCTATCT 1431
Db      |||||
Qy 1485 ACTCCGTTAATTTAGCATCCCTAAGGCTGCTGTGTCCCAACCGAACTGAGCGCCATTT 1544
Db      |||||
Qy 1432 CGATGCTGTACTCTTGACGAGAAATGAAAAGGTTGTATTAAAGAACTATCAGGACATGGTTG 1491
Db      |||||
Qy 1545 CCATGTTGTTATCTGACAGAGTACGACAAAGTGTGTGTTGAAAATAATATCAGGAGATGGTG 1604
Db      |||||
Qy 1492 TGGAGGGTTGTGGGTGTCGCT 1512
Db      |||||
Qy 1605 TGGAGGGGTGCGGATGCGCT 1625
Db      |||||

RESULT 8
US-11-136-527-6238
; Sequence 6238, Application US/11/136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6238
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6238

Query Match      13.0%; Score 201; DB 7; Length 600;
Best Local Similarity 78.2%; Pred. No. 5.4e-48;
Matches 240; Conservative 1; Mismatches 66; Indels 0; Gaps 0;

Qy 1206 AGCTGTAAAGACACCCCTTTGTAGTGGACTTTCAGTGACGCTGGGTTGGAATGACTGGATT 1265
Db      |||||
Qy 1266 GTGGCTCCCCGGGGTATCACGCTTTTACTGCCACCGAGAAATGCCCTTTTCTCTGGCT 1325
Db      |||||
Qy 79 GTGGCCCCWCCAGGCTACCAGGCTTCTACTGCCACCGGGGACTGTCCCTTTCCACTGGCG 138
Db      |||||
Qy 1326 GATCATCTGAACCTCCACTAATCATGCCATTTGTTTCAGACGTTGGTCAACTCTGTTAACTCT 1385
Db      |||||
Qy 139 GRCCACTCAACTCAACCAATCATGCCATTTGTGAGACCCCTGGTCAACTCGTTAATCT 198
Db      |||||
Qy 1386 AAGATTCCTAAGGCATGCTGTGTCGCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTT 1445
Db      |||||
Qy 199 AGCATCCCTAAGGCTTGTGTGTCGCCACCGAACTGAGCGCAATTTCCATGTTGTATCTG 258
Db      |||||
Qy 1446 GACGAGATGAAGGTTGTATTAAAGAACTATCAGGACATGTTGTGGAGGGTGTGGG 1505
Db      |||||
Qy 259 GACGAGTACGACAGGTGGTGTGAAAATAATATCAGGAGATGTTGGTGGAGGGGTGGCGGA 318
Db      |||||
Qy 1506 TGTGCT 1512
Db      |||||
Qy 319 TGGCGCT 325
Db      |||||

RESULT 9
US-11-051-568-16
```

/ Sequence 16, Application US/11051568
/ Publication No. US20050255141A1
/ GENERAL INFORMATION:
/ APPLICANT: OPPERMAN, HERMANN
/ OZKANAK, ERGIN
/ KUBERASAMPATH, THANGAVEL
/ RUEGER, DAVID C.
/ PANG, ROY H.L.
/ TITLE OF INVENTION: OSTEOGENIC DEVICES
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: TESTA, HURWITZ & THIBREAU
/ STREET: 125 HIGH STREET
/ CITY: BOSTON
/ STATE: MASSACHUSETTS
/ COUNTRY: U.S.A.
/ ZIP: 02110
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/11/051,568
/ FILING DATE: 04-Feb-2005
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 10/321,799
/ FILING DATE: 17-DEC-2002
/ APPLICATION NUMBER: US 09/148,925
/ FILING DATE: 8-SEP-1998
/ APPLICATION NUMBER: US 08/449,699
/ FILING DATE: 24-MAY-1995
/ APPLICATION NUMBER: US 08/147,023
/ FILING DATE: 1-NOV-1993
/ APPLICATION NUMBER: US 07/841,646
/ FILING DATE: 21-FEB-1992
/ APPLICATION NUMBER: US 07/827,052
/ FILING DATE: 28-JAN-1992
/ APPLICATION NUMBER: US 07/579,865
/ FILING DATE: 7-SEP-1990
/ APPLICATION NUMBER: US 07/621,849
/ FILING DATE: 4-DEC-1990
/ APPLICATION NUMBER: US 07/621,988
/ FILING DATE: 4-DEC-1990
/ APPLICATION NUMBER: US 07/810,560
/ FILING DATE: 20-DEC-1991
/ APPLICATION NUMBER: US 07/569,920
/ FILING DATE: 20-AUG-1990
/ APPLICATION NUMBER: US 07/600,024
/ FILING DATE: 18-OCT-1990
/ APPLICATION NUMBER: US 07/599,543
/ FILING DATE: 18-OCT-1990
/ APPLICATION NUMBER: US 07/616,374
/ FILING DATE: 21-NOV-1990
/ APPLICATION NUMBER: US 07/483,913
/ FILING DATE: 22-FEB-1990
/ APPLICATION NUMBER: US 07/179,406
/ FILING DATE: 08-APR-1988
/ APPLICATION NUMBER: US 07/232,630
/ FILING DATE: 15-AUG-1988
/ APPLICATION NUMBER: US 07/315,342
/ FILING DATE: 23-FEB-1989
/ APPLICATION NUMBER: US 07/660,162
/ FILING DATE: 22-FEB-1991
/ APPLICATION NUMBER: US 07/422,699
/ FILING DATE: 17-OCT-1989
/ APPLICATION NUMBER: US 07/422,613
/ FILING DATE: 17-OCT-1989
/ APPLICATION NUMBER: US 07/422,623
/ FILING DATE: 17-OCT-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DIANA M. STEEL

/ REGISTRATION NUMBER: 43,153
/ REFERENCE/DOCKET NUMBER: STK-001CP6C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617/248-7000
/ TELEFAX: 617/248-7100
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 525 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: YES
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..516
/ OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "CMP2B-1"
/note= "CMP2B-1 - FUSION"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-051-568-16
Query Match 12.5%; Score 192.8; DB 7; Length 525;
Best Local Similarity 76.6%; Pred. No. 1.2e-45;
Matches 236; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 1206 AGCTGTAAGACACACCCCTTTGTAGTGGACTTCAGTGACGTGGGTGGAATGACTGGATT 1265
DB 211 AACTGCCGGCGCCACTCGCTCTATGTGACTTCACGATGTGGCTGGAATGACTGGATT 270
QY 1266 GTGGCTCCCCGGGGTATCACGCCCTTTTACTGCCACGAGAAATGCCCTTTCTCTGGCT 1325
DB 271 GTGGCCCCACACAGGCTACACAGCCCTTCTACTGCCATGCGAATGCCCTTTCCCGCTAGCG 330
QY 1326 GATCATCTGAATCCCAATCATGCCATTTGTTGAGCTTGTGAGCTTGTGTAACCTCT 1385
DB 331 GATCACTTTCAACAGCACCAACACCGCCGTGGTGCAGACCCCTGGTGAACCTCTGTCAACTCC 390
QY 1386 AAGATTCCCTAAGGCATGCTGTCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTT 1445
DB 391 AAGATCCCTAAGGCTTGTGCTGCCACCGAGCTGTCCGCATCAGCATGCTGTACCTG 450
QY 1446 GACGAGATGAAAGGTTGTATTAAAGAACTATACAGGACATGTTGTGGAGGGTTGTGGG 1505
DB 451 GACGAGATGAGAGGTGCTGCTGAGAACTACACAGGAGATGGTAGTAGAGGGCTGCGGC 510
QY 1506 TGTGCGTA 1513
DB 511 TGCGGCTA 518
RESULT 10
US-11-136-527-6467
/ Sequence 6467, Application US/11136527
/ Publication No. US20050287570A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William M
/ TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
/ FILE REFERENCE: 031896-041000 (AM101086)
/ CURRENT APPLICATION NUMBER: US/11/136,527
/ CURRENT FILING DATE: 2005-05-25
/ PRIOR APPLICATION NUMBER: US 60/574,294
/ PRIOR FILING DATE: 2005-05-26
/ NUMBER OF SEQ ID NOS: 362830
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 6467
/ LENGTH: 1400
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-11-136-527-6467
Query Match 10.3%; Score 159.6; DB 7; Length 1400;

Best Local Similarity 81.8%; Pred. No. 7.2e-36;
Matches 180; Conservative 3; Mismatches 37; Indels 0; Gaps 0;

Qy 1324 CTGATCATCTGAACCTCACTAATCATGCAATGTTTCAGACGTTGGTCAACTCTCTTAACT 1383
Db 1 CTGATCATCTGAACCTCACTAATCATGCAATGTTTCAGACGTTGGTCAACTCTCTTAACT 60

Qy 1384 CTAGATCTCTTAAGGCGATGCTGCTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACC 1443
Db 61 CCAAAATCCCTTAAGGCGATGCTGCTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACC 120

Qy 1444 TTGACGAGATGAAGAGGTTGTTATTAAGAACTATCAGGACATGTTGTGGAGGTTGTG 1503
Db 121 TAGATGAAGAGGTTGTTATTAAGAACTATCAGGACATGTTGTGGAGGTTGTG 180

Qy 1504 GGTGTGCTAGTACAGCAAAATTAATATACATAATATATA 1543
Db 181 GGTGTGCTAGTACAGCAAAATTAATATACATAATATATA 220

RESULT 11

US-10-816-768-90
; Sequence 90, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Wei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 2.0
; SEQ ID NO 90
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: H2487
US-10-816-768-90

Query Match 8.0%; Score 124.4; DB 6; Length 405;
Best Local Similarity 64.8%; Pred. No. 5.6e-26;
Matches 201; Conservative 0; Mismatches 106; Indels 3; Gaps 1;

Qy 1208 CTGTAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACTGTGATTGT 1267
Db 81 CTGTAAGAGACACGAGCTGTATGTACGCTCCGAGACCTGGGCTGGCAGGACTGGATCAT 140

Qy 1268 GGCTCCCCGGGGTATCAGCGCTTTTACTGCCAGGAGATGCCCTTTCTCTCGGTGA 1327
Db 141 CGCGCCTTGAAGGCTACGCGGCTTACTGTGAGGGGGAGTGTGCTTCCCTCTGAATC 200

Qy 1328 TCATCTGAATCCCACTAATCATGTCATGTTTCAGAGCTTGTTCAACTCTGTAACTC--- 1384
Db 201 CTACATGAACCCACACACAGCCATCGTCGACGCTGTGTCCACTTCATCAACCCGGA 260

Qy 1385 TAAGATCTCTAAGCATGCTGTGTCGCCAGAGAACTCAGTGTCTATCTCGATGCTGTACCT 1444
Db 261 AACGGTGCCCAAGCCCTGCTGTGCGCCACGACGCTCAGCGCTATCTCCGCTCTACTT 320

Qy 1445 TGACGAGATGAAGGTTGTATTAAGAACTATCAGGACATGTTGTGGAGGTTGTGG 1504
Db 321 CGATGACAGCTCCAAACGTCATCCTGAAGAAATACGAAGACATGTGTGTCGAAGCTTGTGG 380

Qy 1505 GTGTGCGTAG 1514
Db 381 CTGCAGATAG 390

RESULT 12

US-10-131-826A-341

; Sequence 341, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deenoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 341
; LENGTH: 1252
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-341

Query Match 8.0%; Score 123.6; DB 6; Length 1252;
Best Local Similarity 60.4%; Pred. No. 1.7e-25;
Matches 204; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

Qy 1199 TAAGTCCAGCTGTAAAGAGACACCCCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGA 1258
Db 845 TAAGAACCTCTGCCACCGCTCACCAGCTATTCACTTCGGGACCTGGGTTGGCACA 904

Qy 1259 CTGATGTTGCTCCCGGGGTATCAGCGCTTTTACTGCCACGAGAAATGCCCTTTTCC 1318
Db 905 GTGATCAITGCCCGGAGGGTTTCATGGCAATTTACTGCCATGAGAGTGTCCCTTCTC 964

Qy 1319 TCTGGCTGATCATCTGAACCTCCCAATATCATGCAATTTTTCAGAGCTTTGGTCAACTCTGT 1378
Db 965 ACTGACCATCTCTCAACAGCTCCCAATATGCTTTTCATGCAAGCCCTGATGATCGCT 1024

Qy 1379 TAATCTTAAGATTCCTTAAGCATGCTGTGTGCCGACAGAACTCAGTGTATCTCGATGCT 1438
Db 1025 TGACCCAGAGATCCCGGAGGCTGTGTATATCCCAAGCTGTCTCCCATTTCCATGCT 1084

Qy 1439 GTACCTTGACGAGATGAAGAGTTGTATTAAAGAACTATCAGGACATGGTTGTGAGGG 1498
Db 1085 CTACGAGCAATAATGACATGTCTTCTAGGACATTTAGACATGGTAGTGATGA 1144
Qy 1499 TTGTGGGTGCTGTAGTACAGCAAAATTAATAACATAA 1536
Db 1145 ATGTGGGTGTGGTAGGATGTGAGAAATGGGAATAGAA 1182

RESULT 13

US-11-091-334-1
; Sequence 1, Application US/11091334
; Publication No. US20050244867A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, et al.
; TITLE OF INVENTION: Growth Factor HTER36
; CURRENT APPLICATION NUMBER: US/11/091,334
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/557,393
; PRIOR FILING DATE: 2004-03-30
; PRIOR APPLICATION NUMBER: 10/117,178
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 09/357,905
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 08/827,336
; PRIOR FILING DATE: 1997-03-26
; PRIOR APPLICATION NUMBER: 60/014,098
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41)..(1132)
; OTHER INFORMATION:
US-11-091-334-1

Query Match 7.9%; Score 122; DB 9; Length 1212;
Best Local Similarity 60.1%; Pred. No. 4.8e-25;
Matches 203; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
Qy 1199 TAAGTCAGCTGTAGAGACACCCCTTTGTACGTGACTTTCAGTGAGCTGGGTGGAATGA 1258
Db 820 TAAGAACCTCTGCCACCCGTCACGACTATTCAATTAACCTTCGGGACCTGGGTGGCACAA 879
Qy 1259 CTGGAATTGGCTCCCGGGGTATCAGCCCTTTTACTGCCAGGAGAAATGCCCTTTTCC 1318
Db 880 GTGGATCATTTGCCCAAGGGGTTCATGGCAATTTACTGCCATGGAGAGTGTCCCTTCTC 939
Qy 1319 TCTGGCTGATCATCTGAACTCCACTTAATCATGCCATTTGTCAGAGCTTGGTCAACTCTGT 1378
Db 940 ACTGACCATCTCTCAACAGCTCCATTTATGCTTTTCAAGCCCTGATGATGCCGT 999
Qy 1379 TAACTCTAAGATCTTAAAGGCAATGCTGTGCCGACAGAACTCACTGCTATCTGATGCT 1438
Db 1000 TGACCCAGAGATCCCGGCTGTGTATCTCCCAAGCTGTCTCCCAATTTCCATGCT 1059
Qy 1439 GTACCTTGACGAGATGAAGAGTTGTATTAAAGAACTATCAGGACATGGTTGTGAGGG 1498
Db 1060 CTACGAGGACAAATGACAAATGTCAATCTACGACATTTATGAAGACATGGTAGTCATGA 1119
Qy 1499 TTGTGGGTGCTGTAGTACAGCAAAATTAATAACATAA 1536
Db 1120 ATGTGGGTGTGGTAGGATGTGAGAAATGGGAATAGAA 1157

RESULT 14

US-11-136-527-3392
; Sequence 3392, Application US/11136527

; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3392
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3392
Query Match 7.9%; Score 122; DB 7; Length 1764;
Best Local Similarity 64.1%; Pred. No. 5.8e-25;
Matches 195; Conservative 3; Mismatches 103; Indels 3; Gaps 1;
Qy 1209 TGTAAAGACACCCCTTTGTACGTGACTTTCAGTGACGTGGGTGGAATGACTGGATTGTG 1268
Db 316 TGCAAGAGACATGAGCTTTACGTGAGCTTCAGGACCTCGGATGGCAGACGAGATCATC 375
Qy 1269 GCTCCCGGGGTATCAGCCCTTTTACTGCCAGGAGAAATGCCCTTTTCTCTGGCTGAT 1328
Db 376 GCWCCAAAGGCTAGCGTGCCAACTATTGTGACGGAGAGTGTCTCTCCCTCAATGCA 435
Qy 1329 CATCTGAACCTCCACTTAATCATGCCATTTGTCAGACGTTGGTCAACTCTGTTAACTTAAG 1388
Db 436 CACATGATGCCACCAACCCAGCCATTGTACAGACTTTGGTCCACCTTATGAATCCCGAG 495
Qy 1389 ---ATTCTAAGGCATGCTGTGTCGCCGACAGAACTCAGTGTCTATCTGATGCTGACCTT 1445
Db 496 TACGTCCCAAAACCATGCTGGCGACCAACCAACTGGAATGCCATCTCGGTTCTTTACTTC 555
Qy 1446 GACGAGATGAAGAGTTGTATTAAAGAACTATCAGGACATGGTTGTGAGGGTTGTGGG 1505
Db 556 GACGACAACTCCAATGTCATCTTGAANAATACAGGAACAATGGTTGTGAGAGCTTGTGGA 615
Qy 1506 TGTC 1509
Db 616 TGTC 619
RESULT 15
US-11-051-568-33
; Sequence 33, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; OZKAYNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H. L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568

FILING DATE: 04-Feb-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/321,799
FILING DATE: 17-DEC-2002
APPLICATION NUMBER: US 09/148,925
FILING DATE: 8-SEP-1998
APPLICATION NUMBER: US 08/449,699
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: US 08/147,023
FILING DATE: 1-NOV-1993
APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/827,052
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: US 07/579,865
FILING DATE: 7-SEP-1990
APPLICATION NUMBER: US 07/621,849
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/621,988
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/810,560
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 07/569,920
FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 07/600,024
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/599,543
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/616,374
FILING DATE: 21-NOV-1990
APPLICATION NUMBER: US 07/483,913
FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
FILING DATE: 08-APR-1988
APPLICATION NUMBER: US 07/232,630
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 07/315,342
FILING DATE: 23-FEB-1989
APPLICATION NUMBER: US 07/660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,613
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,623
FILING DATE: 17-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..314
OTHER INFORMATION: /note= "CONSENSUS PROBE"
SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Search completed: January 10, 2006, 23:47:16
Job time : 233 secs

Query Match 7.7%; Score 119; DB 7; Length 314;
Best Local Similarity 66.8%; Pred. No. 1.8e-24;
Matches 185; Conservative 0; Mismatches 89; Indels 3; Gaps 1;

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 19:43:19 ; Search time 4466 Seconds
(without alignments)
16206.811 Million cell updates/sec

Title: US-10-801-648-1
Perfect score: 1547
Sequence: 1 ggggactcttggaacttgca.....aatacataaatatatata 1547

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	981.4	63.4	983	10	AY418812 Homo sapi
3	825.8	53.4	903	5	BX431362 BX431362
4	816.6	52.8	890	5	BX424086 BX424086
5	763.8	49.4	977	10	AY418814 Mus muscu
6	699.2	45.2	724	8	CV804617 AGENCOURT
7	695	44.9	711	10	AY418813 Pan trogl
8	683.8	44.2	727	5	BU625617 UI-H-FGI-
9	683	44.1	711	7	CN396138 170004241
10	673.8	43.6	769	8	CX755622 AGENCOURT
11	664.4	42.9	841	8	DN117475 1117145 M
12	644.8	41.7	830	8	DN117122 1116761 M
13	623.6	40.3	1001	5	BX432994 BX432994
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15	607	39.2	648	3	BM683313 UI-E-EJ1-
16	606.4	39.2	649	3	BQ184625 UI-E-EJ1-
17	605.2	39.1	674	3	BM674840 UI-B-EJ0-
18	597	38.6	642	3	BM929343 UI-E-EJ1-
19	585	37.8	649	3	BQ186599 UI-B-EJ1-
20	579.4	37.5	581	3	BP276858 BP276858
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22	552	35.7	881	5	BU444424 603213309

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	25	525.8	34.0	529	3	BM717570	BM717570	UI-E-EJ0-
	26	522	33.7	544	1	AA488503	AA488503	ab39c02.r
	27	497.2	32.1	511	1	AI492136	AI492136	tg12e01.x
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	29	497	32.1	529	2	BF416123	BF416123	UI-R-CA0-
	30	493.6	31.9	746	7	CV736172	CV736172	1061.e7.5
	31	484.4	31.3	521	1	AA190917	AA190917	zp83h03.r
	32	482.2	31.2	536	1	AA436230	AA436230	zv23h06.r
	33	480.4	31.1	497	1	AA883895	AA883895	am26h03.s
	34	469.2	30.3	580	2	BG149658	BG149658	nad31h05.
	35	469	30.3	483	1	AI084926	AI084926	qf17h06.x
	36	467	30.2	515	1	AA436231	AA436231	zv23h06.s
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	40	456.6	29.5	614	9	AZ655571	AZ655571	1M0530C11
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	44	440	28.4	441	1	AA181547	AA181547	zp51a05.s
	45	439	28.4	469	2	BF409439	BF409439	UI-R-CA1-

ALIGNMENTS

RESULT 1
CR618407
LOCUS
DEFINITION
full-length cDNA clone CS0DE003YB10 of Placenta of Homo sapiens (human).
ACCESSION
CR618407
VERSION
CR618407.1 GI:50499214
KEYWORDS
HTC; CNSLT_CDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2394)
AUTHORS
Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE
2 (bases 1 to 2394)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)
COMMENT
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
location/Qualifiers
source
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/census="CS0DE003YB10"
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/plasmid="pCMVSPORT_6"

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Query Match 100.0%; Score 1547; DB 4; Length 2394;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	TGCCCCCAGCGGAGCCTGCTTTCGCCCATCTCCGAGCCCCACCGCCCTTCGACTCTCTCGGCCT	120
Db	97	TGCCCCCAGCGGAGCCTGCTTTCGCCCATCTCCGAGCCCCACCGCCCTTCGACTCTCTCGGCCT	156
Qy	121	TGCCCGGACACTGAGACGCTGTTTCCAGCGTGAAAGAGAGACTCGCGCGCCGCGCACCCCGG	180
Db	157	TGCCCGGACACTGAGACGCTGTTTCCAGCGTGAAAGAGAGACTCGCGCGCCGCGCACCCCGG	216
Qy	181	GAGAAGGAGGAGGCAAAAGAAAGGAAACGGACAATTCGCTCTTTGCGCCAGAGTCTTTTGACC	240
Db	217	GAGAAGGAGGAGGCAAAAGAAAGGAAACGGACAATTCGCTCTTTGCGCCAGAGTCTTTTGACC	276
Qy	241	AGAGTTTTCATGTGACGCTCTTTTCAAATGGAAGTGTCCCGCGTGTCTTTTAGACGGA	300
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Qy	301	CTCGCGTCTCTCTAAAGGTCGACCATGTGTGCGCGGACCCGCGTGTCTTTAGCGTTGCTGC	360
Db	337	CTCGCGTCTCTCTAAAGGTCGACCATGTGTGCGCGGACCCGCGTGTCTTTAGCGTTGCTGC	396
Qy	361	TTCCCCAGGTCCTCTCTGCGCGCGCGGTGGCTCTGTTTCGAGACTCGGCGCGCAGGAAGT	420
Db	397	TTCCCCAGGTCCTCTCTGCGCGCGCGGTGGCTCTGTTTCGAGACTCGGCGCGCAGGAAGT	456
Qy	421	TGCGGGCGGCGTGTCTGCGGCGCGCCCTCATCTCCAGCCCTCTGACGAGGTCTCTGAGCGAGT	480
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Qy	661	ACCATGAGAAATCTTTTGGAGAACTTACCAGAAACGAGTGGGAAACAAACCCGAGAGTTCT	720
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Qy	721	TCCTTAATTTAAGTTCTATCCCCACGGAGAGTTTATCACTCAGCAGAGCTTCAGGTTT	780
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Qy	781	TCCGAGAACAGATCGAATGCTTTTAGAAAAACAATAGAGTTTCATCACCGGAATTAATA	840
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Db	877	TTTATGAAATCATAAACCTTCACACGCCACTCGAAATTTCCCGTGCACACAGACTTTTGG	936
Qy	901	ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG	960
Db	937	ACACGAGTTGGTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTG	996
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Db	1117	ATGAACA	CAGCTGCTGCACAGATAAGGCCATTGCTAGTAACTTTTGGCCATGCGAAAG	1176
Qy	1141	GGCATCTCTCCACAAAGAGNAAAGCTCAAGCCCAACAAACACGCGGAAACGCCTTA		1200
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Qy	1201	AGTCCAGCTGTAAAGAGACACCCCTTTGACGTGGACCTTCAGTGCAGTGGGGTGGAAATGACT		1260
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Qy	1261	GGATTGTGGCTCCCCCGGGGTATCACGCCCTTTTACTGCGCACGGAGAATGCCCTTTTCCTC		1320
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Qy	1441	ACCTTGACGAGAAATGAAAGGTTGTATTAAGAAGCACTATCAGGACATGTTTGTGCGAGGTT		1500
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Db	1537	GTGGGTGTCGCTAGTACAGCAAAATTAATACATATATATATA	1583	
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DEFINITION	Homo sapiens BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.			
ACCESSION	AY418812			
VERSION	AY418812.1	GI:39774772		
KEYWORDS	GSS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			
	1 (bases 1 to 983)			
	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL	Science 302 (5652), 1960-1963 (2003)			
PUBMED	14671302			
REFERENCE				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			
	2 (bases 1 to 983)			
	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
TITLE	Direct Submission			
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.			
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ORIGIN	/locus_tag="HCM682"			

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Query Match      63.4%; Score 981.4; DB 10; Length 983;
Best Local Similarity 99.9%; Pred. No. 1.8e-264;
Matches 982; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 CCGGACCCGCTGCTTCTAGCGTTGCTGCTTCCCGAGTCTCTCTGGCGCGCGGCTG 60

QY 391 GCCTGTTCCGAGTGGCGCGCAGAGTTGCGCGCGCGCTGCTGCGCGCGCGCTCAT 450
DB 61 GCCTGTTCCGAGTGGCGCGCAGAGTTGCGCGCGCGCTGCTGCGCGCGCGCTCAT 120

QY 451 CCCAGCCTCTGACAGAGTCTTCCAGAGTTCAGTTCGGCTGCTCAGCATGTCGCGC 510
DB 121 CCCAGCCTCTGACAGAGTCTTCCAGAGTTCAGTTCGGCTGCTCAGCATGTCGCGC 180

QY 511 TGAACACAGAGACCCACCCCGACGAGCGCGTGTGCGCGCGCTTACATGCTAGACCTGT 570
DB 181 TGAACACAGAGACCCACCCCGACGAGCGCGTGTGCGCGCGCTTACATGCTAGACCTGT 240

QY 571 ATCGAGGACCTCAGTTCAGCGCGGCTCACCGCGCGCGAGCACCGGTTGAGAGGCGAG 630
DB 241 ATCGAGGACCTCAGTTCAGCGCGGCTCACCGCGCGCGAGCACCGGTTGAGAGGCGAG 300

QY 631 CCAGCGGAGCCAACTGTGCGCAGCTTCCACATGAAGATCTTTGGAAGAACTACACAG 690
DB 301 CCAGCGGAGCCAACTGTGCGCAGCTTCCACATGAAGATCTTTGGAAGAACTACACAG 360

QY 691 AAACAGTGGGAAACAAACCCCGAGATCTTCTTTAAATTAAGTTCTATCCCGAGG 750
DB 361 AAACAGTGGGAAACAAACCCCGAGATCTTCTTTAAATTAAGTTCTATCCCGAGG 420

QY 751 AGTTTATCCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGTGTCTTAGGAA 810
DB 421 AGTTTATCCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGTGTCTTAGGAA 480

QY 811 ACAATAGCAGTTTCCATCAGCGAAATTAATTAATTAATTAATTAATTAATTAATTA 870
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QY 871 ACTGAAATTTCCCGTGACAGACTTTTGGACACAGGTTGTTGAATCAGATGCAAGCA 930
DB 541 ACTGAAATTTCCCGTGACAGACTTTTGGACACAGGTTGTTGAATCAGATGCAAGCA 600

QY 931 GGTGGGAAGTTTGAATGTCACCCCGCTGTGATGCGGTGGAATGCAAGGACAGCA 990
DB 601 GGTGGGAAGTTTGAATGTCACCCCGCTGTGATGCGGTGGAATGCAAGGACAGCA 660

QY 991 ACCATGGATTCGTGTTGGAAGTGGCCCACTTGGAGGAGAAACAAGTGTCTCCAAGAGAC 1050
DB 661 ACCATGGATTCGTGTTGGAAGTGGCCCACTTGGAGGAGAAACAAGTGTCTCCAAGAGAC 720

QY 1051 ATGTTAGGATAGCAGGTTCTTGGCACCAAGATGAACAACAGTGTGTCACAGATAAGGCCAT 1110
DB 721 ATGTTAGGATAGCAGGTTCTTGGCACCAAGATGAACAACAGTGTGTCACAGATAAGGCCAT 780

QY 1111 TGCTAGTAATCTTTGGCCATGATGGAAGAGGGGATCTCTCCACAAAAGAGAAAAACGTC 1170
DB 781 TGCTAGTAATCTTTGGCCATGATGGAAGAGGGGATCTCTCTCCACAAAAGAGAAAAACGTC 840

QY 1171 AAGCCAAACACAAACAGCGGAACCGCTTAAGTCCAGCTGTGAAGAGACACCCCTTTGTAGG 1230
DB 841 AAGCCAAACACAAACAGCGGAACCGCTTAAGTCCAGCTGTGAAGAGACACCCCTTTGTAGG 900

QY 1231 TGGACTTCAGTACGCTGGGGTGGATGACTGGAATGTGGCTCCCGGGGATTCACGCT 1290
DB 901 TGGACTTCAGTACGCTGGGGTGGATGACTGGAATGTGGCTCCCGGGGATTCACGCT 960

QY 1291 TTTACTGCCACGAGAAATGCCCT 1313
DB 961 TTTACTGCCACGAGAAATGCCCT 983

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RESULT 3
BX431362
LOCUS
DEFINITION BX431362 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE003YB10
5-PRIME, mRNA sequence.
ACCESSION BX431362
VERSION BX431362
KEYWORDS BX431362.2 GI:47009531
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 903)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30781021.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 10041.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?n=CS0BAG011ZG10_CS01039_1&c=10041.
f.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE003YB10"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo (dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 53.4%; Score 825.8; DB 5; Length 903;
Best Local Similarity 97.6%; Pred. No. 1.1e-220;
Matches 858; Conservative 0; Mismatches 19; Indels 2; Gaps 2;

QY 598 CACCCGCCCCAGACACCGGTTGGAGAGGGGAGCCAGCCGACGACACACTGTGGCAGCT 657
DB 7 CTCCTCCGCCCCANACCCCGGTTGGGGGGGCGCAGCCGAGGCC-ACACTGTGGCAGCT 65

QY 658 TCACCATGAAGAACTTTTGAAGAACTACCAAGAAACAGTGGGAAACAAACCCGAGAT 717
DB 66 TCACCATGAAGAACTTTTGAAGAACTACCAAGAAACAGTGGGAAACAAACCCGAGAT 125

QY 718 TCTCTTTAAATTAAGTTCTATCTCCACGAGGAGTTTATCACCTCAGCAGGTTTCAGG 777
DB 126 TCTCTTTAAATTAAGTTCTATCTCCACGAGGAGTTTATCACCTCAGCAGGTTTCAGG 185

QY 778 TTTTCGGAACAGATGCAAGTGTCTTAGGAAACATAGCAGTTTCCATCAGCAATTA 837
DB 186 TTTTCGGAACAGATGCAAGTGTCTTAGGAAACATAGCAGTTTCCATCAGCAATTA 245

QY 838 ATATTTATGAATCATATAAAGCTCAACAGCCAACTCGAAATTCGCCGTGACCACTTT 897
DB 246 ATATTTATGAATCATATAAAGCTCAACAGCCAACTCGAAATTCGCCGTGACCACTTT 305

QY 898 TGGACACAGGTTGTTGAATCAGAAATGCAAGCAGGTGGGAAAGTTTGTATGTACCCCG 957

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Db 306 TGGACACACGAGTGTGTGAATCAGATGCAAGCAGGTGGGAAGTGTGATGTCAACCCCG 365
Qy 958 CTGTGATGCGGTGAGCTGTCACAGGACACGCCAACCATGATGATGATGATGATGATGATG 1017
Db 366 CTGTGATGCGGTGAGCTGTCACAGGACACGCCAACCATGATGATGATGATGATGATGATG 425
Qy 1018 ACTTGGAGGAGAAACAGGTGCTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGACCC 1077
Db 426 ACTTGGAGGAGAAACAGGTGCTCTCCAGAGACATGTTAGGATAAGCAGGTCTTTGACCC 485
Qy 1078 AAGATGAACACAGCTGGTGCACAGATAAGGCCATTTAGTAACTTTTGGCCATGATGAA 1137
Db 486 AAGATGAACACAGCTGGTGCACAGATAAGGCCATTTAGTAACTTTTGGCCATGATGAA 545
Qy 1138 AAGGCGATCTCTCCACAAAGAGAGAAACGTCGAAGCCAAACACAAACAGCGGAAACGCC 1197
Db 546 AAGGCGATCTCTCCACAAAGAGAGAAACGTCGAAGCCAAACACAAACAGCGGAAACGCC 605
Qy 1198 TTAAGTCCAGCTGTAAAGAGACACCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATG 1257
Db 606 TTAAGTCCAGCTGTAAAGAGACACCTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATG 665
Qy 1258 ACTGATGTGTGGTCCCGGGGTATCAAGCCTTTTACTGCAAGGAAATGCCCTTTTC 1317
Db 666 ACTGATGTGTGGTCCCGGGGTATCAAGCCTTTTACTGCAAGGAAATGCCCTTTTC 725
Qy 1318 CTCTGGCTGATCATCTGAACCTCCACTAATCATGCCATTGTTTCAGACGTTGGTGCATCTG 1377
Db 726 CTCTGGCTGATCATCTGAACCTCCACTAATCATGCCATTGTTTCAGACGTTGGTGCATCTG 785
Qy 1378 TTAAGTCTAAGATCTTAAGGCATGCTGTGTCGACAGAACTCAGTGCTATCTCGATGC 1437
Db 786 TTAAGTCTAAGATCTTAAGGCATGCTGTGTCGACAGAACTCAGTGCTATCTCGATGC 845
Qy 1438 TGTACCTTGACGAGATGAAAGGTTGTATTAAGAACT 1476
Db 846 TGTACCTTGACGAGATG-AAAGGTTGTATTAAGAACT 883
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RESULT 4
BX424086 890 bp mRNA linear EST 03-MAY-2004
LOCUS BX424086 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE003YB10
DEFINITION 5-PRIME, mRNA sequence.
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ACCESSION BX424086
VERSION BX424086.2
KEYWORDS EST.
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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1 (bases 1 to 890)
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```
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
```

```
Full-length cDNA libraries and normalization
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Unpublished (2001)
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On May 13, 2003 this sequence version replaced gi:30659639.
```

```
Contact: Genoscope
```

```
Genoscope - Centre National de Sequencage
```

```
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
```

```
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
```

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 10041.f

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?c=CS1DE001ZF080P1&c=10041.f>.

Location/Qualifiers

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/mol_type="mRNA"

FEATURES
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/issue_type="PLACENTA"  
/clone_lib="Homo sapiens PLACENTA"  
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."
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ORIGIN

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Query Match 52.8%; Score 816.6; DB 5; Length 890;  
Best Local Similarity 97.3%; Pred. No. 4.3e-218;  
Matches 832; Conservative 16; Mismatches 2; Gaps 2;  
Qy 1 GGGGACTTCTTGAACCTTGCAGGGAGAAATACTTGCACACCCCACTTTTGCGCCGTTC 60  
Db 37 GGGGACTTCTTGAACCTTGCAGGGAGAAATACTTGCGRCCCACTTTTGCGCCGTTC 96  
Qy 61 TCCCCCAGCGGAGCTCTTTCGCCATCTCCGAGCCCCCAACCGCCCTTCACCTCTCGGCCT 120  
Db 97 TCCCCCAGCGGA-SCTGCTTGGCCATCTCCGAGCCCCCAACCGCCCTTCACCTCTCGGCCT 155  
Qy 121 TCCCCGACACTGAGACGCTGTTCCAGCGTGAAAGAGAGACTCGCGCGCGGCAACCGG 180  
Db 156 TCCCCGACACTGAGACGCTGTTCCAGCGTGAAAGAGAGACTCGCGCGCGGCAACCGG 215  
Qy 181 GAGAAGAGGAGGCAAGAAAGGAAACGACATTCGTCCTTGGCCACAGGTCCTTTGACC 240  
Db 216 GAGAAGAGGAGGCAAGAAAGGAAACGACATTCGTCCTTGGCCACAGGTCCTTTGACC 275  
Qy 241 AGAGTTTTCATGTGACGCTCTTTCAATGGAGCTGTCCCGCGTGTCTTTAGACGGA 300  
Db 276 AGAGTTTTCATGTGACGCTCTTTCAATGGAGCTGTCCCGCGTGTCTTTAGACGGA 335  
Qy 301 CTGCGGTCTCTCTAAAGTTCGACCATGTGGCCGCGGACCCGCTGTCTTACGCTTGTCTGC 360  
Db 336 CTGCGGTCTCTCTAAAGTTCGACCATGTGGCCGCGGACCCGCTGTCTTACGCTTGTCTGC 395  
Qy 361 TTCCCCAGGTCTCTCTCGGCGCGCGCTGSCCTCTGTTTCGAGCTGCGGCCGACGAGT 420  
Db 396 TTCCCCAGGTCTCTCTCGGCGCGCGCTGSCCTCTGTTTCGAGCTGCGGCCGACGAGT 455  
Qy 421 TCGCGCGCGGTCTGTCGCGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT 480  
Db 456 TCGCGCGCGGTCTGTCGCGCGCGCCCTCATCCAGCCCTCTGACGAGTCTCTGACGAGT 515  
Qy 481 TCGAGTTTGGCGTCTCTCAGCATGTTTCGCGCTTGAACAGAGACCCACCCAGCAGGAGC 540  
Db 516 TCGAGTTTGGCGTCTCTCAGCATGTTTCGCGCTTGAACAGAGACCCACCCAGCAGGAGC 575  
Qy 541 CCGTGTGCCCCCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGCGGCTCAC 600  
Db 576 CCGTGTGCCCCCTTACATGCTAGACCTGTATCGCAGGCACTCAGGTGAGCGCGGCTCAC 635  
Qy 601 CCGCCCCAGACACCGGTTGGAGAGGCGCAGCCAGCGGCAACACTGTGTGGCAGCTTCC 660  
Db 636 CCGCCCCAGACACCGGTTGGAGAGGCGCAGCCAGCGGCAACACTGTGTGGCAGCTTCC 695  
Qy 661 ACCATGAAGAAATCTTT-GGAAGAACTACCAAGAACGAGTGGGAAAAAACAACCCGAGATTC 719  
Db 696 ACCATGAAGAAATCTTTGGGAAGAACTACCAAGAACGAGTGGGAAAAAACAACCCGAGATTC 755  
Qy 720 TTCTTTAATTAAGTTCTTATCCCGAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTT 779  
Db 756 TTCTTTAATTAAGTTCTTATCCCGAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTT 815  
Qy 780 TTCCGAGACAGATGCAAGATGCTTTTAGGAAACAATAGCAGTTTCCATCAGGATTAAT 839  
Db 816 TTCCGAGACAGATGCAAGATGCTTTTAGGAAACAATAGCAGTTTCCATCAGGATTAAT 875  
Qy 840 ATTTATGAATCAT 854
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Db      876 ATTTATGAATCATATA 890

RESULT 5
LOCUS   AY418814
DEFINITION Mus musculus BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY418814
VERSION   AY418814.1 GI:39774774
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment.
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gene        /gene="BMP2"
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Best Local Similarity 87.5%; Pred.No. 3.3e-203;
Matches 860; Conservative 0; Mismatches 117; Indels 6; Gaps 2;

Qy      331 CCGGACCCGCTGCTCTTAGCGTGGTCTTCCCGAGTCTCTCTGGCGCGCGCGCTG 390
      Db      1 CCGGACCCGCTGCTCTTAGCGTGGTCTTCCCGAGTCTCTCTGGCGCGCGCGCG 60

Qy      391 GCCTCGTTCCGAGTGGCGCGAGAGTTCGCGCGCGCGTCTGTCGCGCGCGCGCTCAT 450
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Qy      451 CCAGCCCTCTGACGAGTCTTGACGAGTTCGAGTTCGCGCGCGCGTCTGACGATGTCGCG 510
      Db      118 CCGCGCTTCCGAGAGCGTCTTCCGAGTTCGAGTTCGCGCGCGCGTCTGACGATGTTGCG 177

Qy      511 TGAAACAGAGACCCACCCCGAGCGCGCGTCTGCGCGCGCGTCTGACGATGTCGAGCGTGT 570
      Db      178 TGAAACAGAGACCCACCCCGAGCGCGCGTCTGCGCGCGCGTCTGACGATGTCGAGCGTGT 237

Qy      571 ATCCGAGGCACTCAGGTCAGCGCGCGTCTGCGCGCGCGTCTGCGCGCGCGTCTGAGAGGCG 630
      Db      238 ATCCGAGGCACTCAGGTCAGCGCGCGTCTGCGCGCGCGTCTGCGCGCGCGTCTGAGAGGCG 297

Qy      631 CCAGCGGAGCGAAGTCTGCGCGCGTCTGCGCGCGCGTCTGCGCGCGCGTCTGAGAGGCG 690
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Qy      691 AAACGAGTGGGAAACCAACCCGAGGATCTTTCTTTAAATTTAGTTCTATCCCAACGAGG 750
      Db      358 AGATGAGTGGGAAACCAACCCGAGGATCTTTCTTTAAATTTAGTTCTATCCCAACGAGG 417

Qy      751 AGTTTATCACCCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCTTTAGGAA 810
      Db      418 AGTTTCTCACAATCTGCAGAACTCCAGATCTTTCCGAGAACAGATGCAAGATGCTTTAGGAA 477

Qy      811 ACAATAGCAGTTCCTCATCACCAGATTAATATTTATGAATCATATAAACTGCAACAGCCA 870
      Db      478 AC---AGTAGTTTCCAGCACCGAATTAATATTTATGAATCATATAAACTGCAACAGCCA 534

Qy      871 ACTGAAATCCCGTGACAGACTTTTGGACACAGAGTTGGTGAATCAGAAATGCAAGCA 930
      Db      535 ACTTGAATTTCTGTGACAGACTTATTTGGACACAGAGTTGGTGAATCAGAAATGCAAGCA 594

Qy      931 GGTGGAAAGTTTGATGTCAACCCCGCTGATGCGGTGGAGTCTGCAAGGACAGCCA 990
      Db      595 AGTGGAGAGCTTCGAAGTCAACCCCGCTGATGCGGTGGAGTCTGCAAGGACAGCCA 654

Qy      991 ACCATGGAATTCGTGTGAAGTGGCCCACTTTGGAGGAGAAACAGGTGTCTCAAGAGAC 1050
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Qy      1051 ATGTTAGGATAAGCAGGTCTTTTGCAACCAAGATGAACACAGCTGGTTCACAGATAAGGCCAT 1110
      Db      715 ATGTTAGGATAAGCAGGTCTTTTGCAACCAAGATGAACACAGCTGGTTCACAGATAAGGCCAT 774

Qy      1111 TGCTAGTAACCTTTGGCCATGATGAAAGGCGATCTCTTCCACAAAAGAGAAAACGTC 1170
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Qy      1171 AAGCAACAAACAAACAGCGGAAACCCCTTAAGTCCAGCTGTAAAGAGACACCCCTTTGTACG 1230
      Db      835 AAGCAACAAACAAACAGCGGAAACCCCTTAAGTCCAGCTGTAAAGAGACACCCCTTTGTACG 894

Qy      1231 TGGACTTCAGTGCAGTGGGGTGGAAATGATGCTGGATTTGGCTCCCCCGGGGTATCAGCCT 1290
      Db      895 TGGACTTCAGTGCAGTGGGGTGGAAATGATGCTGGATTTGGCTCCCCCGGGGTATCAGCCT 954

Qy      1291 TTTACTGCCACGAGAAATGCCCT 1313
      Db      955 TTTACTGCCACGAGAGTGTCT 977

RESULT 6
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LOCUS   AGENCOURT_36361580 NIH MGC_280 Homo sapiens cDNA clone
DEFINITION IMAGE:7503800 5', mRNA sequence.
ACCESSION CV804617
VERSION   CV804617.1 GI:55747583
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 724)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT  Contact: Daniela S. Gerhard, Ph.D.
         Office of Cancer Genomics
         National Cancer Institute / NIH
         Bldg. 31 Rm10A07 Bethesda, MD 20892
         Email: cgsapbs-re@mail.nih.gov
         Tissue Procurement: Meri Firpo
         cDNA Library Preparation: Express Genomics
         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
         DNA Sequencing by: Agencourt Bioscience Corporation
         Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
 Plate: L1AM15873 row: h column: 06
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 Location/Qualifiers
 1. 724

FEATURES

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 /clone_lib="NIH MGC 280"
 /note="Organ: Blastocyst; Vector: pExpress-1; Site_1: EcoRV; Site_2: NotI; RNA obtained from pluripotent cell line derived from blastocyst inner cell mass (cell line HSP-6, NIH Registry designation UC06. Positive for OCT4 expression by rtPCR, positive for SSEA-3, SSEA-4, Tra-1-81, Tra-1-60 by immunofluorescence. Negative for SSEA-1 by immunofluorescence Passage 62. cDNA was primed using oligo-dr primer:
 5'-PGACTGTTAGATCGGAGCGCGGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25 kb resulted in an average insert size of 1.8 kb. This primary library is non-normalized (normalized primary library is NIH_MGC 281) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene Collection library."

ORIGIN

Query Match 45.2%; Score 699.2; DB 8; Length 724;
 Best Local Similarity 98.8%; Pred. No. 4.7e-105;
 Matches 715; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

576 AGGCACTCAGGTGCGCGGTCTACCCGCCAGACACCGGTTGGAGGCGCAGCCAGC 635
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 1 AGGCACTCGGTGCGCGGTCTACCCGCCAGACACCGGTTGGAGGCGCAGCCAGC 60

636 CGAGCCAACTGTGCGGAGCTTCACCATGAAGAATCTTTGGAAGAACTACCGAAACG 695
 Db |
 61 CGAGCCAACTGTGCGGAGCTTCACCATGAAGAATCTTTGGAAGAACTACCGAAACG 120

696 AGTGGGAAACACCGGAGATCTCTTTAAATTTAGTTCTATCCCGGAGGAGCTTT 755
 Db |
 121 AGTGGGAAACACCGGAGATCTCTTTAAATTTAGTTCTATCCCGGAGGAGGTT 180

756 ATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCTTTAGGAAACAAT 815
 Db |
 181 ATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCTTTAGGAAACAAT 240

816 AGCAGTTTCCATCAGCGAATTAATTTATGAATATATAAACTGCAACAGCCAACTCG 875
 Db |
 241 AGCAGTTTCCATCAGCGAATTAATTTATGAATATATAAACTGCAACAGCCAACTCG 300

876 AAATTCCTCCGTCACAGACTTTTGGACACAGGTTGGTGAATCAGATGCAAGCAGGTGG 935
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 301 AAATTCCTCCGTCACAGACTTTTGGACACAGGTTGGTGAATCAGATGCAAGCAGGTGG 360

936 GAAAGTTTGTATGTACACCCCGCTGTGATCGGTGGACTGCACAGGGACAGCCAACTCAT 995
 Db |
 361 GAAAGTTTGTATGTACACCCCGCTGTGATCGGTGGACTGCACAGGGACAGCCAACTCAT 420

996 GGAATTCGTGGTGGAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCCAAAGACAATGTT 1055
 Db |
 421 GGAATTCGTGGTGGAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCCAAAGACAATGTT 480

1056 AGGATAGCAGGTCTTTGCAACAGATGAACAACAGCTGCTCAGATGAAGCCATTGCTA 1115
 Db |
 481 AGGATAGCAGGTCTTTGCAACAGATGAACAACAGCTGCTCAGATGAAGCCATTGCTA 540

1116 GTAACTTTTGCCCATGATGGAAGGGGATCTCTTCCACAAAGAGAAAAACGTCAAGCC 1175
 Db |
 541 GTAACTTTTGCCCATGATGGAAGGGGATCTCTTCCACAAAGAGAAAAACGTCAAGCC 600

Qy 1176 AACACAAACAGCGGAAACCGCTTAAGTCCAGCTGTAAAGACACACCTTTGTAGCTGAC 1235
 Db |
 601 AACACAAACAGCGGAAACCGCTTTAAGTCCAGCTGTAAAGACACACCTTTGTAGCTGAC 660

1236 TTCACTGACGTGGGTGGAATGACTGATTTGTGCTCCCCGGGTATCACGCTTTTAC 1295
 Db |
 661 TTCACTGACGTGGGTGGAATGACGGATTTGTGCTCCCCGGGG-ATCAGCCTTTTAC 719

1296 TGCC 1299
 Db |
 720 TGCC 723

RESULT 7
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 LOCUS Pan troglodytes BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCSSION AY418813
 KEYWORDS Pan troglodytes (chimpanzee)
 SOURCE GSS.
 ORGANISM AY418813.1 GI:39774773
 Pan troglodytes

REFERENCE 1 (bases 1 to 711)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 711)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT These sequences were made by sequencing genomic exons and ordering
 them based on alignment.

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gene

ORIGIN

Query Match 44.9%; Score 695; DB 10; Length 711;
 Best Local Similarity 98.2%; Pred. No. 7.1e-184;
 Matches 698; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 670 AATCTTTGGAGAACTACCGAAACGAGTGGGAAACACCCGAGATTCTTCTTAATT 729
 Db |
 1 AATCTTTGGAGAACTACCGAAACGAGTGGGAAACACCCGAGATTCTTCTTAATT 60

730 TAAGTTCTATCCCCAGGAGGAGTCTATCACTCAGCAGAGCTTCAGGTTTTCGAGAAC 789
 Db |
 61 TAAGTTCTATCCCCAGGAGGAGTCTATCACTCAGCAGAGCTTCAGGTTTTCGAGAAC 120

790 AGATGCAAGATGCTTTTAGGAAACAATAGCAGTTTCCATCAACGAATTAATATTATGAAA 849
 Db |
 121 AGATGCAAGATGCTTTTAGGAAACAATAGCAGTTTCCATCAACGAATTAATATTATGAAA 180

850 TCATAAAACCTGCAACAGCCCAACTCGAAATTTCCCGGTGACCAGACTTTTGACACAGGT 909

```

181 TCATAAAACCTGCAACAGCAACTCGAAATCCCGTGACCAAGCTTTTGGACACAGCT 240
910 TGGTGAATCAGATGCAAGCAGGTGGGAAGTTTGTATGTACCCCGCTGTGATCGGT 969
241 TGGTGAATCAGATGCAAGCAGGTGGGAAGTTTGTATGTACCCCGCTGTGATCGGT 300
970 GGAATGACAGGACAGCAACCACTGGAATTCGTGTGGAAGTGGCCCACTTGGAGGAGA 1029
301 GGAATGACAGGACAGCAACCACTGGAATTCGTGTGGAAGTGGCCCACTTGGAGGAGA 360
1030 AACAAGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGGACCAAGATGAACACA 1089
361 AACAAGTGTCTCCAAGAGACATGTTAGGATAAGCAGGTCTTTGGACCAAGATGAACACA 420
1090 GCTGGTCAAGATAGGCCATGCTAGTAACTTTGGCCATGATGGAAGGCGATCCTC 1149
421 GCTGGTCAAGATAGGCCATGCTAGTAACTTTGGCCATGATGGAAGGCGATCCTC 480
1150 TCACAAAAGAGAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCT 1209
481 TCACAAAAGAGAAAACGTCAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCT 540
1210 GTAAGAGACACCTTTGTACGTGGAATTCAGTGAAGTGGGGTGGAAATGATCGATTTGG 1269
541 GTAAGAGACACCTTTGTACGTGGAATTCAGTGAAGTGGGGTGGAAATGATCGATTTGG 600
1270 CTCCTCCCGGGTATCAGCGCTTTTACTGCAAGAGATGCGCTTTTCTCTGGCTGATC 1329
601 CTCCTCCCGGGTATCAGCGCTTTTACTGCAAGAGATGCGCTTTTCTCTGGCTGATC 660
1330 ATCTGAACCTCACTAATCATGCACTGTTTCAAGCGTGGTCAACTCTGTTA 1380
661 ATCTGAACCTCACTAATCATGCACTGTTTCAAGCGTGGTCAACTCTGTTA 711

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RESULT 8
BU625617/c
LOCUS
DEFINITION
  BU625617 UI-H-FGI-bgn-b-18-0-UI.e1 NCI CGAP FGI Homo sapiens cDNA clone
  UI-H-FGI-bgn-b-18-0-UI 3', mRNA sequence.
ACCESSION
  BU625617
VERSION
  BU625617.1 GI:23291832
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
REFERENCE
  1 (bases 1 to 727)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-27, >POLY A#simple repeat (matched complement) 31-61,
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
  Location/Qualifiers
    1..727
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="UI-H-FGI-bgn-b-18-0-UI"

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/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FGI"
/note="Organ: Enchondroma; Vector: p773-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FGI is a normalized cDNA library obtained from a
pool of mRNA from 2 cell lines from Enchondroma tissues.
The library was constructed according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into p773-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is CGGTCACTC. The cell lines were provided by Dr.
James Martin from the University of Iowa.
TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
TAG_LIB=UI-H-FGI
TAG_SEQ=CGGTCACTC"

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ORIGIN

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Query Match      44.2%; Score 683.8; DB 5; Length 727;
Best Local Similarity 99.6%; Pred. No. 1e-180;
Matches 585; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      860 TGCACAGCCCAACTCGAAATTCCTCGTGACACAGACTTTTGGACACACAGGTGGTGAATCA 919
DB      727 TGCACAGCCCAACTCGAAATTCCTCGTGACACAGACTTTTGGACACACAGGTGGTGAATCA 668
QY      920 GAATCGACAGGTGGGAAGTTTGTATGTACACCCCGCTGTGATGCGGTGGACTGCACA 979
DB      667 GAATCGACAGGTGGGAAGTTTGTATGTACACCCCGCTGTGATGCGGTGGACTGCACA 608
QY      980 GGGACACGCCCAACCATGATTCGTGTGGAAGTGGCCCACTTGGAGGAGAAACAAGGTGT 1039
DB      607 GGGACACGCCCAACCATGATTCGTGTGGAAGTGGCCCACTTGGAGGAGAAACAAGGTGT 548
QY      1040 CTCCTCAAGAGACATGTTAGGATAAGCAGTCTTTTGCACCAAGATGAACACAGCTGTGTACA 1099
DB      547 CTCCTCAAGAGACATGTTAGGATAAGCAGTCTTTTGCACCAAGATGAACACAGCTGTGTACA 488
QY      1100 GATAAGGCCATTCGTAGTAACTTTTGGCCATGATGGAAGGGCATCTCTCCACAAAG 1159
DB      487 GATAAGGCCATTCGTAGTAACTTTTGGCCATGATGGAAGGGCATCTCTCCACAAAG 428
QY      1160 AGAAAAACGTCAAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAAGACACA 1219
DB      427 AGAAAAACGTCAAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTAAAGACACA 368
QY      1220 CCTTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACTGGATTTGGCTCCCGCGG 1279
DB      367 CCTTTTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACTGGATTTGGCTCCCGCGG 308
QY      1280 GTATCAGCGCTTTTACTGTCACCGAGAAATGCCCTTTCTCTGGCTGATCATCTGACTC 1339
DB      307 GTATCAGCGCTTTTACTGTCACCGAGAAATGCCCTTTCTCTGGCTGATCATCTGACTC 248
QY      1340 CACTAATCATGCACTTGTTCAGACGTGTGTCAACTCTGTTAACCTTAAGATTCCTTAAGGC 1399
DB      247 CACTAATCATGCACTTGTTCAGACGTGTGTCAACTCTGTTAACCTTAAGATTCCTTAAGGC 188
QY      1400 ATGCTGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGGAGAGATGAATA 1459
DB      187 ATGCTGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGGAGAGATGAATA 128
QY      1460 GGTGTATTAAGAACTATCAGGACATGGTTGTGAGGGTTGTGGGTTCGCTAGTACAG 1519
DB      127 GGTGTATTAAGAACTATCAGGACATGGTTGTGAGGGTTGTGGGTTCGCTAGTACAG 68
QY      1520 CAAAATTAATACATAATATATATATA 1547

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67 CAAAATTAATACATAAATATATATA 40

Db
|||||
CN396138          711 bp  mRNA  linear  EST 16-MAY-2004
LOCUS              1700424182561 GRN_BB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION
ACCESSION          CN396138
VERSION            CN396138.1 GI:47383733
KEYWORDS
SOURCE             EST.
ORGANISM            Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Bradenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Bradenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbradenberger@geron.com
Insert Length: 711 Std Error: 0.00.
Location/Qualifiers
1. .711
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_BB"
/note="oligo dr primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

FEATURES
source

ORIGIN

Query Match      44.1%; Score 683; DB 7; Length 711;
Best Local Similarity 99.3%; Pred. No. 1.7e-180;
Matches 686; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 246 TTTTCCATGTGGACGCTTTTCAATGGACGTGTCGCCGCGTCTCTTAGACGACTGCG 305
Db 18 TTTTCTCTGTGGACGCTTTTCAATGGACGTGTCGCCGCGTCTCTTAGACGACTGCG 77
Qy 306 GTCTCTCTAAAGTCGACCATGTGCGCGGACCGCTCTCTCTTAGGCTTCTGCTTCCC 365
Db 78 GTCTCTCTAAAGTCGACCATGTGCGCGGACCGCTCTCTCTTAGGCTTCTGCTTCCC 137
Qy 366 CAGTCTCTCTGGCGCGCGCTGCTCTCTCGGAGCTGGCGCGCAGGAAGTTGCG 425
Db 138 CAGTCTCTCTGGCGCGCGCTGCTCTCTCGGAGCTGGCGCGCAGGAAGTTGCG 197
Qy 426 CGCGGCTCTGGCGCGCGCTCTATCCAGCCCTCTGACGAGGTCTTGAGCGATTGAG 485
Db 198 CGCGGCTCTGGCGCGCGCTCTATCCAGCCCTCTGACGAGGTCTTTAGCGAGTTGAG 257
Qy 486 TTGCGGCTGCTCAGCATGCTCGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTG 545
Db 258 TTGCGGCTGCTCAGCATGTTTGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTG 317
Qy 546 GTGCCCCCTACATGCTAGACTGTATCGCAGGCACTCAGGTACGCGGGCTCACCGCC 605
Db 318 GTGCCCCCTACATGCTAGACTGTATCGCAGGCACTCGGGTCAAGCGGGCTCACCGCC 377

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Qy 606 CCAGACCACCGTTGGAGAGGGCAGCCAGCGAGCCCAACACTGTGCGCAGCTTCCACCAT 665
Db 378 CCAGACCACCGTTGGAGAGGGCAGCCAGCGAGCCCAACACTGTGCGCAGCTTCCACCAT 437
Qy 666 GAAGAACTTTGGGAAGAACTACCAAGAAACGAGTGGGAAAAACAACCCGAGATTCTTTT 725
Db 438 GAAGAACTTTGGGAAGAACTACCAAGAAACGAGTGGGAAAAACAACCCGAGATTCTTTT 497
Qy 726 AATTTAAAGTTCTATCCCAAGAGAGTTTATACCTCAGCAGAGCTTCAGGTTTCCGA 785
Db 498 AATTTAAAGTTCTATCCCAAGAGAGTTTATACCTCAGCAGAGCTTCAGGTTTCCGA 557
Qy 786 GAAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATTTAT 845
Db 558 GAAACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATTAATTTAT 617
Qy 846 GAAATCATAAACCTGCAACAGCCAACTCGAAATTTCCCGTGACAGACTTTTCGACACC 905
Db 618 GAAATCATAAACCTGCAACAGCCAACTCGAAATTTCCCGTGACAGACTTTTCGACACC 677
Qy 906 AGGTTGTGTAATCAGAATGCAAGCAGGTGGG 936
Db 678 AGGTTGTGTAATCAGAATGCAAGCAGGTGGG 708

RESULT 10
CX755622          769 bp  mRNA  linear  EST 24-JAN-2005
LOCUS              AGENCOURT 41339099 NIH MGC 279 Homo sapiens cDNA clone
DEFINITION          IMAGE:7777348 3', mRNA sequence.
ACCESSION          CX755622
VERSION            CX755622.1 GI:58052278
KEYWORDS            EST.
SOURCE             Homo sapiens (human)
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 769)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: dcgabs-remail.nih.gov
Tissue Procurement: Meri Firpo
cDNA Library Preparation: Express Genomics
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15927 row: n column: 02
High quality sequence stop: 564.
Location/Qualifiers
1. .769
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab host="DH10B Tona"
/clone_lib="NIH MGC 279"
/note="Organ: Blastocyst; Vector: pExpress-1; Site: 1;
EcoRV; Site: 2; NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSF-1.14, NIH Registry designation UC01. Positive for OCT4
expression by rtPCR, positive for SSEA-3, SSEA-4,
Tra-1-81, Tra-1-60 by immunofluorescence. Negative for

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SSEA-1 by immunofluorescence. Passage 35. This line is a subclone of the parental line; the parental line was subcloned to remove aneuploid cells). cDNA was primed using oligo-dT primer.
5'-pGACTAGTCTAGATCGGAGCGCGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25 kb resulted in an average insert size of 1.82 kb. This primary library is normalized (non-normalized primary library is NIH MGC 278) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene Collection library."

ORIGIN

Query Match	43.6%;	Score	673.8;	DB	8;	Length	769;
Best Local Similarity	96.0%;	Pred. No.	6.7e-178;				
Matches	723;	Conservative	0;	Mismatches	27;	Indels	3;
Gaps	3;						

Qy	131	TCGAGCGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGCACCGCGGAGAGAGGAGG	190
Db	1	TCGAGCGCTGTTCCAGCGTGAAGAGAGAGACTGCGCGCGCGCACCGCGGAGAGAGGAGG	60
Qy	191	AGGCAAGAAAGAGACGACATTCGTCCTTGGCCAGGTCCTTTGACGAGTTTTC	250
Db	61	AGGCAAGAAAGAGACGACATTCGTCCTTGGCCAGGTCCTTTGACGAGTTTTC	120
Qy	251	CATGTGGAGCTCTTTCAATGACGTCGCCCGCTGCTTCTTAGACGACTGCGGTCTC	310
Db	121	CATGTGGAGCTCTTTCAATGACGTCGCCCGCTGCTTCTTAGACGACTGCGGTCTC	180
Qy	311	CTAAGAGTCACATGTTGGCGGACCGCTGCTTCTTAGCGTTGCTTCCCGAGGT	370
Db	181	CTAAGAGTCACATGTTGGCGGACCGCTGCTTCTTAGCGTTGCTTCCCGAGGT	240
Qy	371	CTCTCTGGCGGCGGCTGGCTCGTTCGAGAGCTGGGCCGACGAGAGTTCCGCGCGC	430
Db	241	CTCTCTGGCGGCGGCTGGCTCGTTCGAGAGCTGGGCCGACGAGAGTTCCGCGCGC	300
Qy	431	GTCTGTGGCGCGCTCATCCAGCTCTGACGAGTCTGAGCGAGTTGAGTTGG	490
Db	301	GTCTGTGGCGCGCTCATCCAGCTCTGACGAGTCTGAGCGAGTTGAGTTGG	360
Qy	491	GCTGTCTAGCATGTTGGCGCTGAAGACAGAGACCCACCGCGAGGAGCGCGTGGTCC	550
Db	361	GCTGTCTAGCATGTTGGCGCTGAAGACAGAGACCCACCGCGAGGAGCGCGTGGTCC	420
Qy	551	CCCCTACATGCTAGACTGTATCGCAGGCACTGAGTACGCGGCTCACCCGCCCGAG	610
Db	421	CCCCTACATGCTAGACTGTATCGCAGGCACTGAGTACGCGGCTCACCCGCCCGAG	480
Qy	611	CCACCGTTGGAGGGGAGCGGAGCGGACGACGACGCTGTCGCGAGTCCACCATGAGA	670
Db	481	CCACCGTTGGAGGGGAGCGGAGCGGACGACGACGCTGTCGCGAGTCCACCATGAGA	540
Qy	671	ATCTTTGGAAGAACTACCAAGAACGAGTGGGAAACCAACCCGAGAGTCTTCTTAATTT	730
Db	541	ATCTTTGGAAGAACTACCAAGAACGAGTGGGAAACCAACCCGAGAGTCTTCTTAATTT	599
Qy	731	AAAGTTCTATCCCGCAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAAC	790
Db	600	AAAGTTCTATCCCGCAGGAGGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAAC	659
Qy	791	GATGCAAGATGCTTTAGGAAACATAGAGATTTCCATCAGGAAATTAATATTATGAAT	850
Db	660	AATGCGAGATGCTTTCCGAAACATAGAGATTTCCATCAGGAAATTAATATTATGAAT	718
Qy	851	CATAAACCTGCAACAGGCAACTCGAAATTTCC	883
Db	719	CAT-TAACCTGCTACCACTTGAATTTTCC	750

RESULT 11
DN117475/c
LOCUS

DN117475 841 bp mRNA linear EST 15-FEB-2005

DEFINITION 1117145 MARC 4PTG Sus scrofa cDNA 3', mRNA sequence.
ACCESSION DN117475
VERSION DN117475.1 GI:59811735
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1 (bases 1 to 841)
AUTHORS Smith,T.P.L., Fekking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Noneman,D.J., Wray,J.B. and Keele,J.W.
TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: HHY8017 row: A column: 20
Seq primer: TAGAAGCACAGTCGAGG.
FEATURES
Location/Qualifiers
1..841
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4PTG"
/note="Vector: pcDNA3.1; Site:1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN

Query Match	42.9%;	Score	664.4;	DB	8;	Length	841;
Best Local Similarity	88.2%;	Pred. No.	3e-175;				
Matches	733;	Conservative	0;	Mismatches	97;	Indels	1;
Gaps	1;						

Qy	718	TCTCTTTAAATTTAAGTTCTATCCCGCGGAGGAGTTTATCACTTCAGCAGAGCTTCAGG	777
Db	841	TTTTTTTTTAAATTTAAGTTCTCTGTCCTCCCGCGGAGGAGTTTATCACTTCAGCAGAGCTTCAGG	782
Qy	778	TTTTCCGAGAA CAGATGCAAGATGCTTTAGGAAACAAATAGCAGTTTCCATCACCGAATTA	837
Db	781	TCTTTCCGGAACAGACACAGGAGACTTTGGATTAACAGTAGCAGTTTCCATCACCGAATTA	722
Qy	838	ATATTTATGAATATCTATAAACTGCAACAGCCAACTCGAAATTCCTCGTGACGACTTT	897
Db	721	ATATTTATGAATATCTATAAACTGCAACAGCCAACTCGAAATTCCTCGTGACGACTTT	662
Qy	898	TGGACACAGGTTGCTGTAATCAGAACTGCAAGCAGTGGGAAAGTTTTCATGTACCCCGG	957
Db	661	TGGACACAGGTTGCTGTAATCAGAACTGCAAGCAGTGGGAGAGCTTCGACGCTCACCCCG	602
Qy	958	CTGTGATCGGTGGAGTCTGCACAGGAGCACGCCAACCATGGATTCGTGTGGAGTGGGCC	1017
Db	601	CTGTGATCGGTGGAGTCTGCACAGGAGTCCGCCAACCCAGGTTCTGTGTGGAGTGGGCC	542
Qy	1018	ACTTGGAGAGAAACAGGTGTCTCAAGAGACATGTTAGGATAGCAGGCTTTTGCACC	1077
Db	541	ACCCGGAGGACAGCCCGGAGGTCTCCAAGAGGATGTGCGGATTAGCAGGCTTTTGCACC	482
Qy	1078	AGATGAACACAGCTGCTCAGAGTAAGCCATTCCTAGTACTTTTGGCCATGATGAA	1137
Db	481	AGATGAGACAGCTGGTCAAAATTAAGACCTTCTAGTCACTTTTCGCCACGATGGA	422
Qy	1138	AAGGCGATCCTCTCCACAAAAGAGAAAAACGTCAGAGCCAAAACAAAACAGCGGAAACGCC	1197

Db 421 AAGGACACCTCTGTGCACAAAAGGGAAAAGCGTCAAGCAAAAACACAAAACAGCGCAAGCGCC 362
QY 1198 TTAAGTCCAGCTGTAAAGAGACACCTTTGTAGTGGACTTCACTGACGTGGGTGGATG 1257
Db 361 TGAATCCAGCTGTAAAGAGACACCTTTGTAGTGGACTTCACTGACGTGGGTGGATG 302
QY 1258 ACTGATTTGTGGCTCCCGCGGGTATCACGCCCTTTTACTGCGACAGGAATGCCCTTTTC 1317
Db 301 ACTGGATGTAGCCCGCGGGTATCATGCTTTTACTGCGACAGGAATGCCCTTTTC 242
QY 1318 CTCTGGCTGATCATGTAACTCCACTAATATGATGCAATTTGTAGACGTGGTCAACTCTG 1377
Db 241 CCCTGGCTGATCATGTAACTCCACTAATATGATGCAATTTGTAGACGTGGTCAACTCTG 182
QY 1378 TTAAGTCTAAAGATTCCTTAAGCATGCTGTGTCGCCGACAGAACTCAGTCTATCTCGATGC 1437
Db 181 TTAAGTCTAAAGATTCCTTAAGCATGCTGTGTCGCCGACAGAACTCAGTCTATCTCGATGC 122
QY 1438 TGTACCTTTGACGAGAAATGAAAGGTGTGTTAAAGAACTATCAGGACATGTTGTGGAGG 1497
Db 121 TGTACCTTTGACGAGAAATGAAAGGTGTGTTAAAGAACTATCAGGACATGTTGTGGAGG 62
QY 1498 GTTGTGGGTGCTGTAGTACAGCAAAAT-TAAATACATAAATATATATATATA 1547
Db 61 GTTGTGGGTGCTGTAGTACAGCAAAATGAAAGGTGTGTTAAAGAACTATATATATATA 11

RESULT 12

DN117122 830 bp mRNA linear EST 15-FEB-2005
LOCUS 1116761 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION DN117122

VERSION DN117122.1 GI:59811382

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 830)
AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonnenan,D.J., Wray,J.B. and Keele,J.W.

TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages

JOURNAL Unpublished (2003)

COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smithem@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.

Plate: HHY8017 row: A column: 20

Seq primer: GTAATACGACTCACTATAGG.

FEATURES

source 1..830

Location/Qualifiers

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 4PIG"

/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;

Library made with combined RNA from day-10, day-13,

day-15, day-25, and day-30 whole embryos."

ORIGIN

Query Match 41.7%; Score 644.8; DB 8; Length 830;
Best Local Similarity 88.2%; Pred. No. 1e-169;
Matches 737; Conservative 0; Mismatches 92; Indels 7; Gaps 3;

QY 140 GTTCCAGCGTGAAGAACAGAGACTGCGCGCGCGACCCCGGAGAACAGAGAGGACCAAGA 199
Db 1 GTTCCCTGCGTGGGAGAGAACTGCCGCGCGCGACCCCGGAGAGAGAGAGAGGCGCA 60
QY 200 AAAGGAAACGGAACATTCGGTCCCTTGGCGCAGGTCTTTGACCCAGAG-TTTTTCATGTGGA 258
Db 61 A---GGAAGGAAACCGCGTCCCTGTGCGCAGGTCTTCAGTCAGAGCTTTTTCATGTGGA 117
QY 259 CGCTCTTTCAATGACGTGTCCCGCGTGTCTTTAGACGAGTGCCTTCCCTAAAGGT 318
Db 118 GGCTCTTTCAATGACGTGTCCCGCGTGTCTTTAGACGAGTGTGCGGTCTCTCTAAAGGT 177
QY 319 CGACCATGTGTGGCGGACCGCGTGTCTTTAGAGTTTGTGCTTCCCGCAGGTCTCTCTGG 378
Db 178 CGACCATGTGTGGCGGACCGCGTGTCTTTAGAGTTTGTGCTTCCCGCAGGTCTCTCTGG 237
QY 379 GCGCGCGCGTGGCTCTGTTCCGGAGCTGGCGCGCAGGAAAGTTCGCGCGCGCTCGTGG 438
Db 238 GCGCGCGCGCGACCTCAATCCCGAGCTGGCGCGGAGGAAAGTTC--GCGGCGTCTACTG 294
QY 439 GCGCGCGCTCATCCAGCGCTCTGACGAGTTCCTGACGAGTTCGAGTTGGGTGCTCTCA 498
Db 295 GCCTCTCTCTTCCAGCGCTCGGACGAGCTCTTCAGCGAGTTTGGTTCGCGGTGCTCA 354
QY 499 GCATGTTGGCGCTGAAACAGAGACCCACCCCGACGAGCGCGTGTGCGCCCTTACA 558
Db 355 GCATGTTGGCGCTGAAACAGAGACCCACCCCGACGAGCGCGTGTGCGCCCTTACA 414
QY 559 TGCTAGACCTGTATTCGAGGCACTCAGGTTCAGCGGGCTCACCGCGCCCGACACCGGT 618
Db 415 TGCTGGACCTGTACCGCGCACTTCGGGTTCAGCCAGCGCGCTGCGCCCGACACCGGC 474
QY 619 TGGAGCGGACCGCGGAGCGCACTGTGGCGAGTTCACCATGTAAGATCTTTGG 678
Db 475 TGGAGCGGACCGCGGAGCTTGGCCAAACCGTGGCGAGCTTCCACACAGAAATCTTTGG 534
QY 679 AAGAACTTACAGAAACAGAGTGGGAAACAAACCGGAGATCTCTTTAAATTTAAGTTCTA 738
Db 535 AAGAACTTCCAGAAATAGTGTGAAACAAACCGCGCGCTTCTTTAAATTTAAGTTCTG 594
QY 739 TCCCCAGGAGGAGTTTATCACCTTCAGCAGAGCTTCAGGTTTTCGGAACAGATGCAAG 798
Db 595 TCCCCAGGAGGAGTTTATCACCTTCAGCAGAGCTTCAGGTTTTCGGAACAGACAGG 654
QY 799 ATGCTTTAGGAAACATAGCAGTTTCCATCAGCAATTAATATTTATGAATCATATAAC 858
Db 655 AGACTTTGGATAACAGTAGCAGTTTCCATCAGCAATTAATATTTATGAATCATATAAC 714
QY 859 CTGCAACAGCAACTCGAAATTTCCCGTGACCAAGCTTTTGGACACAGGTTGGTGAATC 918
Db 715 CTGCAACAGCAACTCCAGTTCCCGTGACCAAGCTTTTGGACACAGGTTGGTGAATC 774
QY 919 AGAATGCAACAGGTTGGGAAAGTTTGTGATGTCAACCCCGCTGTGATCGGTGGACT 974
Db 775 CGAATGCCAGAGTGGGAGAGCTTCGACGTCAACCCCGCTGTGATCGGTGGACT 830

RESULT 13

EX432994/c

LOCUS

DEFINITION

EX432994 Homo sapiens PLACENTA

3-PRIME, mRNA sequence.

ACCSSION

EX432994

VERSION

EX432994.2

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1001)

Li,W.B., Gruber,C., Jesse,J., and Polayes,D.

Full-length cDNA libraries and normalization

EX432994 1001 bp mRNA linear EST 04-MAY-2004

LOCUS

DEFINITION

EX432994 Homo sapiens PLACENTA

3-PRIME, mRNA sequence.

ACCSSION

EX432994

VERSION

EX432994.2

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1001)

Li,W.B., Gruber,C., Jesse,J., and Polayes,D.

Full-length cDNA libraries and normalization

JOURNAL
COMMENT

Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30781178.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 10041.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BA1008ZG11_CS00759_1&c=10041.f.

FEATURES
source

Location/Qualifiers
1..1001
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE003YB10"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 40.3%; Score 623.6; DB 5; Length 1001;
Best Local Similarity 93.1%; Pred. No. 9.7e-164;
Matches 707; Conservative 0; Mismatches 45; Indels 7; Gaps 5;

QY 794 GCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCAGAAATAATATTATGAATCAT 853
DB 1001 GCAAAATTTTAAAGGAACAATAGACAGATTTCCTCCCGGAATTATATTTATGAATCAAT 942
QY 854 AAAACTTCACAGCAGCAACTCGAATT--CCCGTGACCAGACTTTTGAC--ACCAGGT 909
DB 941 AAACTTGCACACAGCAAACTGGAATTTCCCGGTGACAGGTCTTTTGGCCACCACAGGT 882
QY 910 TGGTCAATCAGAACTCAAGCAGTGGGAAAGTTTGTATGTC-ACCCCGCTGTGTATGCGG 968
DB 881 TGTTAATCAAAATCAAGAAGTGGGAAAGTTTGTATGTCACCCCGCTGTGTATGCGG 822
QY 969 TGGACTGCACAGGACAGCCCAACCATGGATTCTGTTGGAGTGGCCCACTTGGAGGAG 1028
DB 821 TGGACTGCACAGGAACAGCCCAACCATGGATTCTGTTGGAGTGGCCCACTT-GAGGAG 763
QY 1029 AAACAAGGTGCTTCAAGGACATGTTAGGATAAGCAGTCTTTCGACCACAGATGAACAC 1088
DB 762 AAACAAGGTGCTTCAAGGAAACATGTTAGGATAAGCAGTCT-TNGCACCACAGATGAACAC 704
QY 1089 AGCTGTGCACAGTAAGGCCATTGCTAGTAACTTTTGGCCATGATGGAAAGGGCATCT 1148
DB 703 AGCTGTGCACAGTAAGGCCATTGCTAGTAACTTTTGGCCATGATGGAAAGGGCATCT 644
QY 1149 CTCACAAAGAGAAAACGTCAGCAGCAAAACAACACAGCGGAAACGCCCTTAAGTCCAGC 1208
DB 643 CTCACAAAGAGAAAACGTCAGCAGCAAAACAACACAGCGGAAACGCCCTTAAGTCCAGC 584
QY 1209 TGTAAAGACACCCCTTTGACGTGACCTTCAGTGACGTGGGTGGAATGACCTGGATTGTG 1268
DB 583 TGTAAAGACACCCCTTTGACGTGACCTTCAGTGACGTGGGTGGAATGACCTGGATTGTG 524
QY 1269 GCTCCCGGGGTATCACGCCCTTTTACTGCACGGGATGCCCTTTTCCCTCTGCGTCAAT 1328
DB 523 GCTCCCGGGGTATCACGCCCTTTTACTGCACGGGATGCCCTTTTCCCTCTGCGTCAAT 464
QY 1329 CATCTGAATCCCACTAACTCATGCCATTTGTTACAGAGTTGGTCAACTCTGTTAACTCTAAG 1388
DB 463 CATCTGAATCCCACTAACTCATGCCATTTGTTACAGAGTTGGTCAACTCTGTTAACTCTAAG 404

QY 1389 ATTCTAAGGCATGCTGTGTCCTCCGACGAACTCAGTGTCTATCTCGATGCTGTACCTTCAC 1448
DB 403 ATTCTAAGGCATGCTGTGTCCTCCGACGAACTCAGTGTCTATCTCGATGCTGTACCTTCAC 344
QY 1449 GAGAAATGAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGTGGAGGTTGTGGGTGT 1508
DB 343 GAGAAATGAAAGGTTGTTAATAAGAACTATCAGGACATGTTGTGTGGAGGTTGTGGGTGT 284
QY 1509 CGCTAGTACACAAATTAATAACATACATAATATATATA 1547
DB 283 CGCTAGTACACAAATTAATAACATACATAATATATATA 245

RESULT 14
AW33267/c

LOCUS AW33267 666 bp mRNA linear EST 31-JAN-2000
DEFINITION xz89f02.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2871387 3,
similar to gb:M22489 BONE MORPHOGENETIC PROTEIN 2 PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION AW33267 GI:5835926

VERSION AW33267.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 666)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgsabbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 455.

FEATURES

source

1..666
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2871387"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI-CGAP Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneID8
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 40.1%; Score 619.6; DB 1; Length 666;
Best Local Similarity 97.7%; Pred. No. 1.2e-162;
Matches 639; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 894 CTTTGGACACAGGTTGTTGAATCAGAAATGCAACAGGTGGGAAAGTTTGTATGATCTACC 953
DB 666 CTTTGGACACAGGTTGTTGAATCAGAAATGCAACAGGTGGGCAAGTTTGTATGATCTACC 607

```
Qy 954 CCGCTGTGATGCGTGGACTGCACAGGACACGCCAACCATGATTCGTGCGAAGTG 1013
Db |||||
Qy 606 CCGCTGTG-ATGCGGTGACTAGCAGGACACGCCAACCATGATTCGTGCGTAAAGTG 548
Db |||||
Qy 1014 GCCCATTGGAGGAGAAACAAGGTGTCTTCCAGAGACATGTTAGGATAAGCAGGTCTTTG 1073
Db |||||
Qy 547 GCCCATTGGAGTAGAACAAGGTGTCTTCCAGAGACATGTTAGGATAAGCAGGTCTTTG 488
Db |||||
Qy 1074 CACCAAGATGAACACAGCTGTGTACAGTAAAGGCCATGCTAGTAACTTTTGGCCATGAT 1133
Db |||||
Qy 487 CACCAAGATGAACACAGCTGTGTACAGTAAAGGCCATGCTAGTAACTTTTGGCCATGAT 428
Db |||||
Qy 1134 GGAAGAGGATCTCTTCCACAAAGAGAGAAAAGTCAAGCCAAACACAAACACGCGGAAA 1193
Db |||||
Qy 427 GGAAGAGGATCTCTTCCACAAAGAGAGAAAAGTCAAGCCAAACACAAACACGCGGAAA 368
Db |||||
Qy 1194 CGCCTTAAGTCCAGCTGTAAAGAGACACCCCTTTTACGTGGACTTCAGTGACGTGGGGTGG 1253
Db |||||
Qy 367 CGCCTTAAGTCCAGCTGTAAAGAGACACCCCTTTTACGTGGACTTCAGTGACGTGGGGTGG 308
Db |||||
Qy 1254 AATGACTGGATGTGGCTCCCGGGGTATCACGCTTTTACTGCGCAGGAGATGCCCT 1313
Db |||||
Qy 307 AATGACTGGATGTGGCTCCCGGGGTATCACGCTTTTACTGCGCAGGAGATGCCCT 248
Db |||||
Qy 1314 TTTCTCTGGCTGATCATCTGAATCCCACTAATCATGCTTGTTCAGAGCTTGGTCAAC 1373
Db |||||
Qy 247 TTTCTCTGGCTGATCATCTGAATCCCACTAATCATGCTTGTTCAGAGCTTGGTCAAC 188
Db |||||
Qy 1374 TCTGTTAACTCTAAGATTCCTAAGGCATGCTGTGTCCGACAGAACTCAGTGTCTATCTCG 1433
Db |||||
Qy 187 TCTGTTAACTCTAAGATTCCTAAGGCATGCTGTGTCCGACAGAACTCAGTGTCTATCTCG 128
Db |||||
Qy 1434 ATGCTGATCTTGACGAGAAATGAAGTTGTATTAAGAACTATCAGGACATGTTGTG 1493
Db |||||
Qy 127 ATGCTGATCTTGACGAGAAATGAAGTTGTATTAAGAACTATCAGGACATGTTGTG 68
Db |||||
Qy 1494 GAGGTTGTGGGTGTCGCTAGTACAGCAAAATTAATACATATATATATA 1547
Db |||||
Qy 67 GAGGTTGTGGGTGTCGCTAGTACAGCAAAATTAATACATATATATATA 14
Db |||||
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RESULT 15
BM683313/c
LOCUS BM683313 648 bp mRNA linear EST 27-FEB-2002
DEFINITION UI-E-EJ1-aje-m-21-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone
            UI-E-EJ1-aje-m-21-0-UI 3', mRNA sequence.
ACCESSION BM683313
VERSION   BM683313.1 GI:18993209
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE 1 (bases 1 to 648)
            Bonaldo,M.F., Lennon,G. and Soares,M.B.
            Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
PUBMED    8889548
COMMENT   Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
```

The following repetitive elements were found in this cDNA sequence: 22-52, >(TA)n#Simple_repeat (matched complement)
Seq primer: M13 Forward
POLYA=Yes.

Location/Qualifiers
1. 648
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ1-aje-m-21-0-UI"
/tissue_type="fetal eye, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EJ1 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGAATAGCA; eye anterior segment, AATGCCGCAT; optic nerve, CCAATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual system, supported by National Eye Institute (NEI).
TAG TISSUE=human fetal eyes
TAG LIB=UI-E-EJ1
TAG_SEQ=AGAATCAAGA"

ORIGIN

Query Match 39.2%; Score 607; DB 3; Length 648;
Best Local Similarity 99.7%; Pred. No. 4.2e-159;
Matches 607; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 939 AGTTTTCATGTCAACCCCGCTGTGATCGGTGGACTGCACAGGACACGCCAACCATGGA 998
Db |||||
Qy 639 AGTTTTCATGTCAACCCCGCTGTGATCGGTGGACTGCACAGGACACGCCAACCATGGA 580
Db |||||
Qy 999 TTCTGTGTGGAAGTGGCCCACTTGGAGGAGAAAACAAGTGTCTCCAGAGACATGTTAGG 1058
Db |||||
Qy 579 TTCTGTGTGGAAGTGGCCCACTTGGAGGAGAAAACAAGTGTCTCCAGAGACATGTTAGG 520
Db |||||
Qy 1059 ATAAGCAGGCTTTTGCACCAAGATGAACAAGCTGGTCAAGATAAGGCCATTGCTAGTA 1118
Db |||||
Qy 519 ATAAGCAGGCTTTTGCACCAAGATGAACAAGCTGGTCAAGATAAGGCCATTGCTAGTA 460
Db |||||
Qy 1119 ACTTTTGGCCATGATGAAAGGGCATCTCTCCACAAAGAGAAAACGTCAGAGCCAAA 1178
Db |||||
Qy 459 ACTTTTGGCCATGATGAAAGGGCATCTCTCCACAAAGAGAAAACGTCAGAGCCAAA 400
Db |||||
Qy 1179 CACAAACAGCGAAAACGCCCTTAAGTCCAGCTGTAAAGAGACACCCCTTTGACGTGGACTTC 1238
Db |||||
Qy 399 CACAAACAGCGAAAACGCCCTTAAGTCCAGCTGTAAAGAGACACCCCTTTGACGTGGACTTC 340
Db |||||
Qy 1239 AGTCAGCTGGGGTGGAAATGACTGGAATGTGGCTCCCGGGGGTATCAGCGCTTTTACTGTC 1298
Db |||||
Qy 339 AGTCAGCTGGGGTGGAAATGACTGGAATGTGGCTCCCGGGGGTATCAGCGCTTTTACTGTC 280
Db |||||
Qy 1299 CACGAGAAATGCCCTTTTCTCTGCTGATCATCTGAACCTCCACTTAATCATGCCATCTT 1358
Db |||||
Qy 279 CACGAGAAATGCCCTTTTCTCTGCTGATCATCTGAACCTCCACTTAATCATGCCATCTT 220
Db |||||
Qy 1359 CAGAGTTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGATGCTGTGTCCCGCAGAA 1418
Db |||||
Qy 219 CAGAGTTTGGTCAACTCTGTAACTCTTAAGATTCTTAAGGATGCTGTGTCCCGCAGAA 160
Db |||||

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Qy 1419 CTCAGTCTATCTCGATGCTGTACCTTTGACGAGAAATGAAAAGGTTGTATTAAAGAACTAT 1478
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Db 159 CTCAGTCTATCTCGATGCTGTACCTTTGACGAGAAATGAAAAGGTTGTATTAAAGAACTAT 100
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Qy 1479 CAGGACATGGTTGTGGAGGGTTGTGGGTGTCGCTAGTACAGCAAAATTAAATACATAAAT 1538
    |||||
Db 99 CAGGACATGGTTGTGGAGGGTTGTGGGTGTCGCTAGTACAGCAAAATTAAATACATAAAT 40
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Qy 1539 ATATATATA 1547
    |||||
Db 39 ATATATATA 31
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Search completed: January 10, 2006, 23:23:52
Job time : 4473 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2006, 23:24:00 ; Search time 4449 Seconds
(without alignments)
5059.565 Million cell updates/sec

Title: US-10-801-648-2
Perfect score: 2098
Sequence: 1 MVAGTRCILLALLPOVLGG.....NEKVLKNYQDMVVGCGCR 396

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+ptn.model -DEV=xlh
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-DB=GenEmbl -QFMT=fastap -SUFFIX=rgc -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -NORM SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*

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- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sv.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_hg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2098	100.0	1215	6	BD124160 Treatment
2	2098	100.0	1547	6	CQ875282 Sequence
3	2098	100.0	1547	6	CS031823 Sequence

4	2098	100.0	1547	6	CS040775
5	2098	100.0	1547	6	I78455
6	2098	100.0	1547	6	AX775087
7	2098	100.0	1547	8	HUMBMP2A
8	2098	100.0	1581	6	CS038212
9	2098	100.0	1607	6	ARI57708
10	2098	100.0	3526	6	AR447458
11	2095	99.9	1607	6	AR031482
12	2095	99.9	1607	6	AR130859
13	2095	99.9	1607	6	AR353792
14	2092	99.7	1260	6	AR075478
15	2092	99.7	1260	6	I15550
16	2092	99.7	1260	6	I83779
17	2092	99.7	1260	6	AR308031
18	2092	99.7	1260	6	AR350343
19	2092	99.7	1607	6	I08630
20	2092	99.7	2041	8	BC069214
21	2092	99.7	2154	6	CS031821
22	2092	99.7	2154	6	CS040773
23	2092	99.7	2154	6	AX201366
24	2084	99.3	1547	6	CQ728408
25	2043.5	97.4	1314	6	BD003258
26	2022.5	96.4	2148	4	AF041421
27	1948	92.9	2540	9	BC100344
28	1943	92.6	2502	4	DSPMP2
29	1932.5	92.1	1258	9	RATMORPH2A
30	1932.5	92.1	1275	9	RNBMP2
31	1796.5	85.6	1233	6	I62380
32	1796.5	85.6	1233	6	AR492773
33	1687	80.4	1179	5	AY237249
34	1565	74.6	2093	5	XLEMP2
35	1562	74.5	2366	5	XLEMP27
36	1554	74.1	2643	5	CR848433
37	1542	73.5	1992	5	XLEMP222
38	1542	73.5	1992	6	E03670
39	1542	73.5	1992	6	I66400
40	1540	73.4	2630	5	BC100164
41	1532.5	73.0	1120	5	GGHMP2
42	1530	72.9	1940	5	BC092021
43	1511	72.0	14759	6	CQ876148
44	1511	72.0	14759	6	CQ877130
45	1511	72.0	14759	6	CQ880078

ALIGNMENTS

RESULT 1	BD124160	BD124160	1215 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD124160	Treatment of bone loss with osteoblastoma precursor cells.				
DEFINITION	BD124160	Treatment of bone loss with osteoblastoma precursor cells.				
ACCESSION	BD124160	BD124160.1	GI:23219105			
VERSION	BD124160	JP 2002502822-A/13.				
KEYWORDS	BD124160	synthetic construct				
SOURCE	BD124160	synthetic construct				
ORGANISM	BD124160	other sequences: artificial sequences.				
REFERENCE	BD124160	1 (bases 1 to 1215)				
AUTHORS	BD124160	Hollinger, J.O., Win, S.R., Edmondo, P. and Wang, S.S.				
TITLE	BD124160	Treatment of bone loss with osteoblastoma precursor cells				
JOURNAL	BD124160	Patent: JP 2002502822-A 13 29-JAN-2002;				
		OREGON HEALTH SCIENCES UNIVERSITY				
COMMENT	BD124160	OS Artificial Sequence				
		PN JP 2002502822-A/13				
		PD 29-JAN-2002				
		PF 10-FEB-1999	JP 2000530221			
		PR 10-FEB-1998	US 60/074240, 12-FEB-1998	US	60/074451	PI
			JEFFREY O HOLLINGER, SHELLEY R WIN, FRANK EDMONDO, SHU SI WANG PC			
			A61K35/12, A61B17/56, A61F2/38, A61K9/00, A61K38/22, A61L27/00, PC			
			A61L29/00			
			PC A61P19/00, A61P19/10, C07K14/51, C12N5/10, C12N15/09, A61K37/24, PC			
			C12N5/00			
			PC C12N15/00			
			CC Description of Artificial Sequence: KS-hBMP-2 plasmid PH			Key

QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
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 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 DB 564 GACCTGTATCGAGGCACTCAGGTCAAGCGGGCTCACCGGCCAGAGACCGGTTGGAG 623
 QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGlnGluSerLeuGluGlu 120
 DB 624 AGGCAGCAGCCGAGGCAACACTGTGCGAGCTTCCACCATGAAGAATCTTTGGAAGAA 683
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 DB 744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTTCCGAGAACAGATGCAAGATGCT 803
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 DB 1284 CACGCTTTTATCTGCACGAGAATGCCCTTTCTCTGCTGATCATCTGAACCTCACT 1343
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RESULT 3
 CS031823
 LOCUS
 DEFINITION

CS031823 1547 bp DNA linear PAT 10-MAR-2005
 Sequence 1329 from Patent WO2005016962.

ACCESSION CS031823
 VERSION CS031823.1 GI:60731673
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Abbas A., Clark H., Ouyang W., Williams M.P., Wood W.I. and Wu, T.D.
 TITLE Compositions and methods for the treatment of immune related diseases
 JOURNAL Patent: WO 2005016962-A 1329 24-FEB-2005;
 Genentech, Inc. (US)
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 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAsnSerGlyArg 40
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 QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
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 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 DB 564 GACCTGTATCGAGGCACTCAGGTCAAGCGGGCTCACCGGCCAGAGACCGGTTGGAG 623
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 QY 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
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 DB 864 ACAGCAACTCGAAATTCCTCGTGACAGACTTTTGGACACAGGTTGGTGAATCAGAT 923
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Db      984  CACGCCAACCATGATTCGTGTGAGAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC  1043
Qy      241  LysArgHisValArgHisSerArgSerLeuHisGlnAenGluHisSerTrpSerGlnIle  260
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Qy      261  ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu  280
Db      1104  AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGGCGCATCTCTCCACAAAGAGAA  1163
Qy      281  LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro  300
Db      1164  AAACGTCACGCCAACACACAAACAGCGGAAACGCCTTAAGTCCAGCTGTAAAGAGACACCCCT  1223
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Db      1224  TTGTACGTGGACTTCAGTGACGTGGGTGGGAATGACTGATTTGTGGCTCCCGCGGGTAT  1283
Qy      321  HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr  340
Db      1284  CACGCCTTTACTGCCAGGAGATGCCCTTTCTCTGGCTGATCATCTGAACTCCACT  1343
Qy      341  AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys  360
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Qy      381  ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg  396
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CS040775      1547 bp      DNA      linear      PAT 22-MAR-2005
LOCUS      Sequence 1329 from Patent WO2005019258.
DEFINITION      CS040775
ACCESSION      CS040775
VERSION      CS040775.1 GI:61848432
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE      1
AUTHORS      Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.
TITLE      Compositions and methods for the treatment of immune related
diseases
JOURNAL      Patent: WO 2005019258-A 1329 03-MAR-2005;
Genentech, Inc. (US)
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/organism="Homo sapiens"
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Alignment Scores:
Pred. No.:      1.84e-135      Length:      1547
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Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      6      Gaps:      0
US-10-801-648-2 (1-396) x CS040775 (1-1547)

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Qy      41  ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet  60
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Qy      161  LeuGlyAenAenSerSerPheHisArgIleAenIleTyrGluIleLysLeuProAla  180
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Qy      201  AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly  220
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||||| 1404 TGTGTCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGATGAAAAGGTT 1463

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Db 1464 GTATTAAAGAACTATCAGACATGTTGTGGAGGTTGTGGGTGTCG 1511

RESULT 5

LOCUS I78455 1547 bp DNA linear PAT 03-APR-1998

DEFINITION Sequence 2 from patent US 5693615.

ACCESSION I78455

VERSION I78455.1 GI:3014609

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1547)

AUTHORS Stone,R.Lee.

TITLE Therapeutic compositions for osteoinduction

JOURNAL Patent: US 5693615-A 2 02-DEC-1997;

FEATURES Location/Qualifiers

source 1..1547

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Pred. No.: 1.84e-135 Length: 1547

Score: 2098.00 Matches: 396

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x I78455 (1-1547)

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Db 384 GCGGCTGGCTGCTTCCGAGCTGGGCGCGCAGAAAGTTTCGGCGCGCTGCTGGCGCGC 443

Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60

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Db 564 GACCTGTATCGAGGACCTCAGTTCAGCGGCTCAGCGGCTCAGCGGCTCAGCGGCTGAG 623

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Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396

Db 1464 GTATTAAAGAACTATCAGACATGTTGTGGAGGTTGTGGGTGTCG 1511

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AX775087 1547 bp DNA linear PAT 09-JUL-2003

LOCUS AX775087

DEFINITION Sequence 403 from Patent WO03038129.

ACCESSION AX775087

VERSION AX775087.1 GI:32486603

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Raponi,M.

TITLE Methods for assessing and treating leukemia

JOURNAL Patent: WO 03038129-A 403 08-MAY-2003;

Ortho-Clinical Diagnostics, Inc. (US)

FEATURES source 1..1547

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ORIGIN

Alignment Scores:

Pred. No.: 1.84e-135 Length: 1547

Score: 2098.00 Matches: 396

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 100.00% Indels: 0
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US-10-801-648-2 (1-396) x AX775087 (1-1547)

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Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuLeuLeuSerMet 60
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1464 GTATTAAAGAACTATCAGGACATGCTGTGTGGAGGTTGTGGTGTGCG 1511

RESULT 7

HUMBMP2A 1547 bp mRNA linear PRI 31-OCT-1994

LOCUS Human bone morphogenetic protein 2A (BMP-2A) mRNA.

DEFINITION M22489

ACCESSION M22489.1 GI:179501

VERSION bone morphogenetic protein.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (sites)

Wozney,J.M., Rosen,V., Celeste,A.J., Mitsock,L.M., Whitters,M.J., Kriz,R.W., Hewick,R.M. and Wang,E.A.

Novel regulators of bone formation: molecular clones and activities

JOURNAL Science 242 (4885), 1528-1534 (1988)

PUBMED 3201241

REFERENCE 2 (bases 1 to 1547)

Wozney,J.M., Rosen,V., Celeste,A.J., Mitsock,L.M., Whitters,M.J., Kriz,R.W., Hewick,R.M. and Wang,E.A.

Unpublished (1989)

JOURNAL

COMMENT Original source text: Human osteosarcoma cell line U-2 OS, cDNA to mRNA, clone hBMP-2A.

[1] sites.

Draft entry and computer readable copy of sequence [1] kindly submitted by R.W. Kriz 10-FEB-1989.

FEATURES

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ORIGIN

Alignment Scores:

Pred. No.: 1.84e-135 Length: 1547

Score: 2098.00 Matches: 396

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x HUMBMP2A (1-1547)

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QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
 Db 384 GCGGCTGGCTCTGTTCCGAGCTGGCGCGCAGAGTTCCGCGCGCGCTGTCGCGCGCGC 443

QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
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QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
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QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
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QY 381 ValLeuLysAsnTyrrGlnAspMetValValGluGlyCysGlyCysArg 396
 Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGGTGTGTGGGTGTGCG 1511

RESULT 8
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 LOCUS Sequence 10 from Patent WO2005016368.
 DEFINITION CS038212
 ACCESSION CS038212
 VERSION CS038212.1 GI:60734760
 KEYWORDS Homo sapiens (human)
 SOURCE

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 1 Sfeir,C., Campbell,P., Jadowiec,J.A. and Kumta,P.
 TITLE Method of inducing biomineralization, method of inducing bone
 regeneration and methods related thereof
 JOURNAL Patent: WO 2005016368-A 10 24-FEB-2005;
 University of Pittsburgh of the Commonwealth System of Hi gher
 Education (US); Carnegie Mellon University (US)
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ORIGIN
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x CS038212 (1-1581)

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QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
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QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrrMetLeu 80
 Db 504 TTGCGCTGTGAACAGAGACCCACCCAGCAGGAGCGCGTGTGCTCCCTACATGCTA 563

QY 81 AspLeuTyrrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db 564 GACCTGTATCGCAGGCACTCAGGTTCAGCGCGGCTCACCGCGCCAGACCCCGTTGGAG 623

QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
 Db 624 AGGCGAGCGCGCGAGCCCAACTGTGGCGCAGTTCACCATGAAGAATCTTTGGAAGAA 683

QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
 Db 684 CTACAGAAACGAGTGGGAAACACACCGGAGATCTCTTTAAATTTAAGTTCTATATCCC 743

QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160

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Db 804 TTAGGAAACAATAGCAGTTTCATCACCGAATTAATATTTATGAATCATAAACCTGCA 863
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Qy 381 ValLeuLysAenTyrGlnAaspMetValValGluGlyCysGlyCysArg 396
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AR157708
LOCUS AR157708 1607 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 3 from patent US 6245889.
ACCESSION AR157708
VERSION AR157708.1 GI:16218701
KEYWORDS
SOURCE Unknown.
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ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1607)
Wang, S.A., Wozney, J.M. and Rosen, V.A.

TITLE BMP-4 products

JOURNAL Patent: US 6245889-A 3 12-JUN-2001;

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ORIGIN

Alignment Scores:

Pred. No.: 1.93e-135 Length: 1607

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x AR157708 (1-1607)

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Qy 41 ProSerSerGlnProSerAaspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
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 DEFINITION Sequence 11 from patent US 6673549.
 ACCESSION AR447458
 VERSION AR447458.1 GI:42675782
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3526)
 AUTHORS Furness, L.M. and Buchbinder, J.L.
 TITLE Genes expressed in C3A liver cell cultures treated with steroids
 JOURNAL Patent: US 6673549-A 11 06-JAN-2004;
 Incyte Corporation; Palo Alto, CA
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US-10-801-648-2 (1-396) x AR447458 (1-3526)

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 VERSION AR031482.1 GI:5945771
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 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1607)
 AUTHORS Israel, D. and Wolfman, N.M.
 TITLE Recombinant bone morphogenetic protein heterodimers
 JOURNAL Patent: US 5866364-A 1 02-FEB-1999;
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ORIGIN

Alignment Scores:

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Query Match: 99.86% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x AR031482 (1-1607)

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Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyGluIleLeuLysProAla 180
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Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 896 ACAGCAACTCGAAATTCCTCCGTGACACAGACTTTTGGACACACAGGTTGGTGAATCAGAT 955
Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 956 GCAAGCAGTGGGAACTTTTGATGTCAACCCCGCTGTGATCGCGTGGACTGSCACAGGA 1015
Qy 221 HisAlaAsnHisGlyPheValValAlaIleHisLeuGluLysGlnGlyValSer 240
Db 1016 CACGCCAACCATGATTCGTGGTGAAGTGCCACCTTGGAGGAGAAACAAGGTGTCTCC 1075
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1076 AAGAGACATGTTAGGATAAGCAGGTCTTTTGACCAAGATGAACAGCTGGTTCACAGATA 1135
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1136 AGGCCATGCTAGTAACCTTTTGGCCATGATGGAAAGAGGCACTCTCTCACAAAGAGAA 1195
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1196 AAGCTCAAGCCAAACACAAACAGCGGAAACGCTTAAGTCAAGCTGTAAGAGACACCT 1255
Qy 301 LeuTyValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTy 320
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Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1376 AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTAACTCTAAGATTCTTAAGGCATGC 1435
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyIleuAspGluAsnGluLysVal 380
Db 1436 TGTGTCCCGCAGAACTCAGTCTATCTCGATGCTGTACCTTGACGAGAAATGAAGAAGTT 1495
Qy 381 ValLeuLysAsnTyTrpGlnAspMetValValGluGlyCysGlyCysArg 396
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RESULT 12
LOCUS AR130859 1607 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6190880.
ACCESSION AR130859
VERSION AR130859.1 GI:14119184
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1607)
AUTHORS Israel, D. and Wolfman, N.M.
TITLE Recombinant bone morphogenetic protein heterodimers, compositions
and methods of use
JOURNAL Patent: US 6190880-A 1 20-FEB-2001;
FEATURES Location/Qualifiers
source 1..1607
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 3,11e-135 Length: 1607
Score: 2095.00 Matches: 395
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.86% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x AR130859 (1-1607)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
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Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaSerSerGlyArg 40
Db 416 GCGGCTGGCGGAGCTGGCGGAGCTGGCGGAGCTGGCGGAGCTGGCGGAGCTGG 475
Qy 41 ProSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
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Qy 61 PheGlyLeuLysGlnArgProThrProSerArgPheAlaValValProProTyMetLeu 80
Db 596 GACCTGTATCCAGGCACTCAGGTCAGCGGGCTCACCGCCAGACCCACCGGTTGGAG 655
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Db      776 ACGGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACACATGCAAGATGCT 835
Qy      161 LeuGlyAsnAsnSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db      836 TTAGGAAACATAGCAGTTTCCATCACCAGATTATATTTATGAATCATATAAACCTGCA 895
Qy      181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db      896 ACAGCAACTCGAAATTCCTCGTACCAGACTTTTGGACACAGGTTGGTGAATCAGAAAT 955
Qy      201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db      956 GCAAGCAGGTGGGAAACTTTTGTATGTCAACCCCGCTGTGTGCGGTGACCTGCACAGGA 1015
Qy      221 HisAlaAsnHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
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Db      1196 AAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAGAGACCCCT 1255
Qy      301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
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Qy      321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db      1316 CACGCTCTTTTACTGCCACGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAACCTCACT 1375
Qy      341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db      1376 AATCATGCCATGTTTCAGACGTGGTCAACTCTGTTAACTCTTAAGATCTTAAGGCATGC 1435
Qy      361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db      1436 TGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACTTGTACGAGAGATGAAAGGTT 1495
Qy      381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
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LOCUS   AR353792 1607 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6593109.
ACCESSION AR353792
VERSION   AR353792.1 GI:33759850
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1607)
AUTHORS Israel D. and Wolfman, N.M.
TITLE   Recombinant bone morphogenetic protein heterodimers, compositions
        and methods of use
JOURNAL Patent: US 6593109-A 1 15-JUL-2003;
        Genetics Institute, Inc.; Cambridge, MA;
        WO; Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 3.11e-135 Length: 1607
Score: 2095.00 Matches: 395
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.86% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x AR353792 (1-1607)

Qy      1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
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Db      416 CGGCTGGCCTCGTTCCGAGCTGGGCGCAGGAGTTCCGCGCGCGCTCTCTGGCGCGC 475
Qy      41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
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Qy      81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db      596 GACCTGTATCCGAGGCACTCAGGTGAGCGGGCTCACCGCGCCAGACACCGCGTTGGAG 655
Qy      101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGlu 120
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Qy      121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db      716 CTACAGAAACGAGTGGGAAACACCCGAGATCTCTCTTTAAATTAAGTTCTATATCC 775
Qy      141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db      776 ACGGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACACATGCAAGATGCT 835
Qy      161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db      836 TTAGGAAACAATAGCAGTTTCCATCACCAGAAATTAATAATTTATGAATCATATAAACCTGCA 895
Qy      181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db      896 ACAGCAACTCGAAATTCCTCGTACCAGACTTTTGGACACAGGTTGGTGAATCAGAAAT 955
Qy      201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db      956 GCAAGCAGGTGGGAAACTTTTGTATGTCAACCCCGCTGTGTGCGGTGACCTGCACAGGA 1015
Qy      221 HisAlaAsnHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
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Db 1256 TTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACTGGATTGTGGCTCCCGGGGTAT 1315
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1316 CACGCCCTTTACTGCCAGGAGATGCCCTTTCTCTGGCTGATCATCTGAATCTCACT 1375
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Db 1436 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAGGTT 1495
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
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LOCUS AR075478 1260 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 4 from patent US 5958441.
ACCESSION AR075478
VERSION AR075478.1 GI:10002228
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Oppermann,H., Ozkaynak,E., Kuberasampath,T., Rueger,D.C. and Pang,R.H.I.
TITLE Devices comprising chondrogenic protein and methods of inducing endochondral bone formation therewith
JOURNAL Patent: US 5958441-A 4 28-SEP-1999;
FEATURES Location/Qualifiers
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Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
DB: 6 Gaps: 0

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Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 129 CCTCATCCAGCCCTCTGACGAGGTCCTGACGAGTTCCGAGTTGCGGCTGCTCAGCATG 188
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
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Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 369 CTACCGAANAACGAGTGGGAAAACACCCGGAGATTCTCTTTAATTTAAGTTCTATCCCC 428
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 429 ACGGAGAGTTTATCACTCAGCAGAGCTTCAGGTTTTCGAGAACACAGATGCAAGTCT 488
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 489 TTAGGAAACAATAGCAGTTTCCATCCCGAATTAATATTTATGAATCATAAAAACCTGCA 548
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Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
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Db 909 TTGTACGTGGACTTCAGTGAGTGGGGTGGAAAGTGAATGTGGTCTCCCGGGGTAT 968
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Db 1089 TGTGTCCGACAGAACTCAGTGCTATCTCGATGTGTACCTTTCAGGAGATGAAGAAGTT 1148
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1149 GTATTAAAGAACTATCAGGATATGTTGTGGAGGTTGTGGGTGTCG 1196

RESULT 15
LOCUS 115550
DEFINITION Sequence 4 from patent US 5468845.
ACCESSION 115550
VERSION 115550.1 GI:1250458
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Oppermann,H., Ozkaynak,E., Kuberasampath,T. and Rueger,D.C.

TITLE Antibodies to osteogenic proteins
JOURNAL Patent: US 5468845-A 4 21-NOV-1995;
FEATURES Location/Qualifiers
source 1..1260
/organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.: 3,73e-135 Length: 1260
Score: 2092.00 Matches: 395
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
DB: Gaps: 0

US-10-801-648-2 (1-396) x I15550 (1-1260)

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QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
DB 69 GCGGCTGGCTCGTTCCGAGCTGGCGCGCAGAAAGTTCCGGCGCGCTCGTGGGCGGC 128
QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
DB 129 CCTCATCCAGCCCTCTGACGAGGTCTGAGCGAGTTCGAGGTTCGGCTGCTCAGCATG 188
QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
DB 189 TTCGCCCTGAAACAGACAGACCCACCCAGCAGCGGAGCGCGTGGTCCCTTACATGCTA 248
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DB 249 GACCTGTATCGCAGGCACTCGGGTTCAGCGGGCTCACCGGCCAGAGACCCCGGTTGGAG 308
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QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
DB 549 ACAGCCAACTCGAAATTCCTCCGTCACCGAGTCTTTTGGACACCCAGGTGGTGAATCAGA 608
QY 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
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Job time : 4475 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2006, 22:09:25 ; Search time 530 Seconds

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Title: US-10-801-648-2

Perfect score: 2098

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Searched: 4996997 seqs, 332346308 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

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12: Geneseqm2004a:*
13: Geneseqm2004bs:*
14: Geneseqm2005a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2098	100.0	1191	10	ADL13511 Osteoarthritis
2	2098	100.0	1215	2	Aaz08554 KS-hBMP-2
3	2098	100.0	1547	2	Aag32851 BMP2. 3/2
4	2098	100.0	1547	2	Aav01679 Bone morph

5	2098	100.0	1547	6	ABK90308	Abk90308 DNA encod
6	2098	100.0	1547	8	ABX76358	Abx76358 Lung canc
7	2098	100.0	1547	8	ACF34481	Acf34481 Gene enco
8	2098	100.0	1547	10	ACF05920	Acf05920 Human bon
9	2098	100.0	1547	10	ADD14609	Add14609 Human src
10	2098	100.0	1547	10	ADE85186	Ade85186 Farnesyl
11	2098	100.0	1547	10	AAD63420	Aad63420 Human bon
12	2098	100.0	1547	10	ABT17041	Abt17041 Human MP2
13	2098	100.0	1547	10	ADL13510	Adl13510 Osteoarth
14	2098	100.0	1547	11	ADN38841	Adn38841 Cancer/an
15	2098	100.0	1547	12	ADH11558	Adh11558 Human bon
16	2098	100.0	1547	12	ADK90635	Adk90635 Human CBM
17	2098	100.0	1547	12	ADO49064	Ado49064 Human deb
18	2098	100.0	1547	13	ADR80231	Adr80231 Bone morph
19	2098	100.0	1547	13	ADQ67125	Adq67125 Human bla
20	2098	100.0	1547	13	ADG73742	Adg73742 Human bon
21	2098	100.0	1547	14	ADW15055	Adw15055 Bone morph
22	2098	100.0	1547	14	ADY15523	Ady15523 DNA encod
23	2098	100.0	1547	14	ADX39020	Adx39020 Human bon
24	2098	100.0	1547	14	ADY81389	Ady81389 Human bon
25	2098	100.0	1547	14	AEA01570	Aea01570 Human bon
26	2098	100.0	1581	14	ADY28715	Ady28715 Human bon
27	2098	100.0	1607	2	AAQ14036	Aaq14036 Human BMP
28	2098	100.0	1607	2	AAQ31869	Aaq31869 Human BMP
29	2098	100.0	1607	2	AAQ41291	Aaq41291 Human BMP
30	2098	100.0	1607	2	AAT64523	Aat64523 Human BMP
31	2098	100.0	1607	2	AAT78941	Aat78941 Human bon
32	2098	100.0	1607	4	AAD16012	Aad16012 Human bon
33	2098	100.0	1607	4	AAC90497	Aac90497 Human BMP
34	2098	100.0	1607	12	ADO40078	Ado40078 Human BMP
35	2098	100.0	3526	12	ADL12282	Adl12282 Human ste
36	2092	99.7	1258	12	ADM80488	Adm80488 Human ost
37	2092	99.7	1258	13	ADO03610	Ado03610 CDNA enco
38	2092	99.7	1260	2	AAQ53143	Aaq53143 Sequence
39	2092	99.7	1260	2	AAT02602	Aat02602 Human CBM
40	2092	99.7	1260	2	AAV15206	Aav15206 Human ost
41	2092	99.7	1260	2	AAZ00231	Aaz00231 Human ost
42	2092	99.7	1260	2	AAZ27581	Aaz27581 Human pre
43	2092	99.7	1260	10	ADJ62679	Adj62679 Human CMB
44	2092	99.7	1260	12	ADE52750	Ade52750 Human ost
45	2092	99.7	2154	6	ABK40276	Abk40276 CDNA enco

ALIGNMENTS

RESULT 1
ADL13511
ID ADL13511 standard; DNA; 1191 BP.
AC ADL13511;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Osteoarthritis-associated polymorphic nucleotide #43.
XX
KW ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
KW joint space narrowing; osteophyte development; joint pain;
KW osteoarthritis; SNP; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO2003054166-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US041225.
XX
PR 20-DEC-2001; 2001US-0342603P.
XX
PA (INCY-) INCYTE GENOMICS INC.
PI Jones KA, Schafer A;
XX

DR WPI; 2003-559141/52.
XX Determining susceptibility of an individual to joint space narrowing,
PT osteophyte development and/or joint pain comprises identifying whether
PT the individual has at least one polymorphism in a polynucleotide encoding
PT a protein.
XX
XX
XX Disclosure; SEQ ID NO 43; 297pp; English.

PS The invention relates to a method of determining susceptibility of an
CC individual to joint space narrowing and/or osteophyte development and/or
CC joint pain comprising identifying whether the individual has at least one
CC polymorphism in a polynucleotide encoding at least one of the protein
CC listed in the specification. The methods, composition and agent are
CC useful for modulating the susceptibility of an individual to joint space
CC narrowing and/or osteophyte development and/or joint pain that is
CC associated with a disease, preferably osteoarthritis. The cell line and
CC the non-human animal are useful for screening for an agent for diagnosing
CC an individual having susceptibility to joint space narrowing and/or
CC osteophyte development and/or joint pain. This sequence corresponds to
CC the polynucleotide encoding a protein listed in the specification. (Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).

SQ Sequence 1191 BP; 296 A; 315 C; 318 G; 262 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.39e-174 Length: 1191
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-801-648-2 (1-396) x ADL13511 (1-1191)

Qy	1	MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly	20
Db	1	ATGTGGCGCGGAGCCCGTGTCTTCTAGCGTGTCTTCCCGAGGTCCTCTCGGCGGC	60
Qy	21	AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaAlaSerSerGlyArg	40
Db	61	CGGCTGGCTCGTTCGGAGCTGGCGCGAGGAGTTCCGGCGGCGCTCTCGGCGCGC	120
Qy	41	ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet	60
Db	121	CCCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTCCGAGTTCCGCTCTCAGCATG	180
Qy	61	PheGlyLeuLeuGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu	80
Db	181	TTCCGCTTGAACAGAGAGACCCACCCCGAGGAGCGCGTGGTCCCGCTACATGCTA	240
Qy	81	AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu	100
Db	241	GACCTGTATCGAGGACATCAGTTCAGCGCGGCTCACCCGCGCCAGACCCAGGTTGAG	300
Qy	101	ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu	120
Db	301	AGGCGAGCCAGCCGAGCCACACCTGTGGCGAGCTTCCACCATGAAGATCTTTGGAGAA	360
Qy	121	LeuProGluThrSerGlyValThrThrArgArgPhePheAsnLeuSerSerIlePro	140
Db	361	CTACAGAAACGAGTGGGAAACAAACCCGGAGATTCCTTTTAATTTAAGTTCTATCCCC	420
Qy	141	ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla	160
Db	421	ACGAGGAGTTTATACCTCTAGCAGAGCTTCAGGTTTCCGAGAACAGATCCAGATGCT	480
Qy	161	LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla	180
Db	481	TTAGGAAACAATAGCAGTTTCCATCCCGAATTAATTTATGAATTCATAAACCCTGCA	540

Qy	181	ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn	200
Db	541	ACGCCAACTCGAAATTCCTCGTGACAGACTTTTGGACACACAGGTTGGTGAATCAGAA	600
Qy	201	AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly	220
Db	601	GCAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGTATCGGTGAGCTGCACAGGA	660
Qy	221	HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer	240
Db	661	CACGCCAACCATGATTCGTGGTGAAGTGCCCACTTGGAGGAGAAACAAGGTGTCTCC	720
Qy	241	LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle	260
Db	721	AAGAGACATGTTAGGATAAGCAGGTCTTTGCACCAAGATGAACACAGCTGTGTACAGATA	780
Qy	261	ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu	280
Db	781	AGGCATTTGCTAGTAATCTTTTGGCCATGATGGAAGAGGCACTCTCTCCACANAGAGAA	840
Qy	281	LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro	300
Db	841	AAAGCTCAGCCAAACACAAACAGCGCAACGCCCTTAAGTCCAGCTGTAAAGACACCCCT	900
Qy	301	LeuTyrValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyr	320
Db	901	TTGTACGTGGACTTCAGTGAGCTGGGTGGAATGACTGGATTTGGCTTCCCGGGGTAT	960
Qy	321	HisAlaPheTyrCysHisGlyGluCysPheProLeuAlaAspHisLeuAsnSerThr	340
Db	961	CAGCCTTTTACTGCCAGCGAGATGCCCCCTTTCTCTGGCTGATCATCTGAACCTCACT	1020
Qy	341	AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysLysIleProLysAlaCys	360
Db	1021	AATCATGCCATTTGTCAGACGTTGGTCAACTCTCTTAACCTTAAGATTCTTAAGGCATGC	1080
Qy	361	CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal	380
Db	1081	TGTGTCCCGACAGAACTCAGTGTCTCTCGATGCTGTACCTTTGACGAGAAATGAAGGTT	1140
Qy	381	ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg	396
Db	1141	GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTCTCGC	1188
RESULT 2			
AAZ08554			
ID	AAZ08554 standard; DNA; 1215 BP.		
XX	AAZ08554;		
AC	AAZ08554;		
XX	18-OCT-1999 (first entry)		
DT	KS-hBMP-2 plasmid vector nucleotide sequence.		
DE	Osteocalcin; osteonectin; osteopontin; bone morphogenic protein; BMP;		
XX	parathyroid hormone receptor; alkaline phosphatase; procollagen; human;		
KW	osteoblast precursor cell; OPC; bony defect; osseous defect;		
KW	traumatic bone loss; congenital insufficiency; malformation;		
KW	osteoporosis; surgical resection; traumatic avulsion; ss.		
XX	Synthetic.		
OS	Homo sapiens.		
XX	WO9939724-A1.		
FN	12-AUG-1999.		
XX	10-FEB-1999; 99WO-US002946.		
PD	10-FEB-1998; 98US-0074240P.		
XX	12-FEB-1998; 98US-0074451P.		
PR	(UYOR-) UNIV OREGON HEALTH SCI.		
XX			
PA			

XX Hollinger JO, Winn SR, Frank E, Wong SC;
 XX WPI; 1999-494212/41.
 XX Composition for treating osseous defects e.g. traumatic bone loss,
 XX congenital insufficiency and/or malformations.
 XX Example 8; Page 32; 81pp; English.
 XX The present invention describes composition (I) for treating osseous
 XX defects comprising a porous matrix and a cell that is committed to an
 XX osteogenic lineage. The composition is useful for healing a bone defects,
 XX especially those caused by osteoporosis, cyst like cavities, surgical
 XX resection, traumatic avulsion and congenital insufficiency. The
 XX compositions assist in the repair and regeneration of bone. Osteoblast
 XX precursor cells (OPC's) boost bone making capability of an ill or aged
 XX individual where OPC's are numerically deficient or functionally
 XX impaired. OPC's can be administered to express BMP to repair bone
 XX defects. The implant is useful for promoting vascular ingrowth and bone
 XX formation, especially in treating bone defects e.g. osteopenic spine. The
 XX composition promotes vascular ingrowth and bone formation without
 XX becoming a barrier to the progression of bone formation. OPC's can be
 XX gently introduced into the cavity without disrupting the cells in the
 XX suspension and they also encourage additional bone formation in the
 XX surrounding bone. The present sequence represents a plasmid vector
 XX containing human bone morphogenic protein 2 (hBMP-2), given in an example
 XX from the present invention

SQ Sequence 1215 BP; 300 A; 326 C; 324 G; 265 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,51e-174 Length: 1215
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-801-648-2 (1-396) x AAQ208554 (1-1215)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
 DB 17 ATGGTGGCGGACCGGTCTCTAGCTTGCTCTCCAGGTCTCTCTGGCGGC 76
 QY 21 AlaAlaGlyLeuValProGlnLeuGlyArgArgPheAlaAlaSerSerGlyArg 40
 DB 77 GCGGCTGGCTCGTTCCGAGCTGGCGCGCAGGAAGTTCCGCGCGCGCTCGTGGCGGC 136
 QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
 DB 137 CCTCATCCAGCCCTCTGACAGGTCTGACGAGTTCGAGTTCGCGCTCTCAGCAG 196
 QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
 DB 197 TTCGGCTGAACAGAGACCCACCCAGCAGCGCGTGGTGGTCCCTACATGCTA 256
 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 DB 257 GACCTGTATCGCAGGCACTCAGTCCAGCGGCTCACCGCGCCAGACCACCGTTGGAG 316
 QY 101 ArgAlaAlaSerArgAlaSerPheValArgSerPheHisGluGluSerLeuGluGlu 120
 DB 317 AGGGCAGCCAGCGCAGCCAACTGTGGCAGCTTCCACCATGAAGAATCTTTGGAGAA 376
 QY 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
 DB 377 CTACCAAGAACGGTGGGAAACACCCGAGATCTTCTTAATTTAAGTCTATCCCC 436
 QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 DB 437 ACGGGAGAGTTTATCACCTCAGCAGAGCTTCAGGTTTTCCGAGAACAGATGCAATGCT 496

QY 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLeuProAla 180
 DB 497 TTAGGAACAATAGCAGTTTCCATCACCGAATTAATTTATGAATCATATAAACCTGCA 556
 QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 DB 557 ACACCAACTCGAAATTCCTCGTGACCCAGACTTTTGGACACACAGGTTGGTGAATCAGAA 616
 QY 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
 DB 617 GCAAGCAGTGGGAAGTTTGTATGTACCCCTGTGATGCGGTGAGCTGCACAGGA 676
 QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
 DB 677 CACGCCAACCATGATTCTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 736
 QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTTPSerGlnIle 260
 DB 737 AAGAGACATGTTAGGATAAGCAGGTCTTTGACCAAGATGAACACAGCTGGTGCACAGATA 796
 QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 DB 797 AGGCATTTGCTAGTAACTTTTGGCCATGATGGAAGGCACTCTCTCCACAAAGAGAA 856
 QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 DB 857 AACGTCAGCCAAACACACACACAGCGGAAACGCTTAAGTCCAGCTGTAAGAGACACCCCT 916
 QY 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTTPIleValAlaProProGlyTyr 320
 DB 917 TTGTACGTGGACTTTCAGTGCAGTGGGTGGTAATGACTGGATTTGTGGCTCCCGGGGTAT 976
 QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 DB 977 CACGCTTTTACTGCCAGGAGATGCCCTTTTCTCTGGCTGATCATCTGAATCCACT 1036
 QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 DB 1037 AATCATGCCATTGTTCCAGCTTGGTCACTCTGTAACTCTAAGATTTCTTAAGGCATGC 1096
 QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 DB 1097 TGTGTCCCGACAGAACTCAGTCTATCTCGATGCTGTACCTTGACGAGAAATGAAGGTT 1156
 QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 DB 1157 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTCTCGC 1204
 RESULT 3
 AAQ32851
 ID AAQ32851 standard; cDNA; 1547 BP.
 XX
 AC AAQ32851;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-MAY-1993 (first entry)
 XX
 DE BMP2.
 XX
 KW Bone; morphogenetic; protein; BMP; growth; vitamin D; systemic;
 KW treatment; dimer; ss.
 XX
 OS Rattus rattus.
 XX
 PN W09221365-Al.
 XX
 PD 10-DEC-1992.
 XX
 PF 26-MAY-1992; 92WO-US004356.
 XX
 PR 05-JUN-1991; 91US-00709621.
 PR 27-MAR-1992; 92US-00856110.
 XX

(PROC) PROCTER & GAMBLE CO.
 Stone RL;
 WPI; 1992-433371/52.
 Synergistic compen. for generating mammalian bone growth - comprises vitamin=D cpd. and bone morphogenetic protein.
 Disclosure; Page 27-29; 44pp; English.
 The sequences given in AAQ32850-56 encode bone morphogenetic proteins (BMP). BMP's increase bone growth and when used in conjunction with vitamin D the level of new bone growth is greater than when a BMP or vitamin D are used alone. The BMP's are administered for systemic treatment at a dose range of 1pg to 100 microg. BMP are active as dimers. (Updated on 25-MAR-2003 to correct PN field.)
 Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.2e-174 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-801-648-2 (1-396) x AAQ32851 (1-1547)

Qy	1	MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly	20
Db	324	ATGGTGGCGGGAGCCCGCTGCTTCTACGCTGTGCTTCTCCCGAGGCTCTCTCGGGCGGC	383
Qy	21	AlaAlaGlyLeuValProGluLeuGlyArgArgGlyPheAlaAlaSerSerGlyArg	40
Db	384	CGGCTGGCCTCGTTCGGAGCTGGCGCGCAGGAAGTTCCGGCGCGCTCTCGGGCGGC	443
Qy	41	ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet	60
Db	444	CCCTCATCCAGCCCTCTGACGAGTCTCTGACGAGTTCGAGCGAGTTCCGCGCTCTCAGCATG	503
Qy	61	PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProTyrMetLeu	80
Db	504	TTCCGCTTGAACAGAGAGACCCACCCCGCAGGAGCGCGGTGCCCCCTCATGCTA	563
Qy	81	AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu	100
Db	564	GACCTGTATCCAGGCACTCAGGTACGCGGGCTCACCCGCCCCAGACCACCGGTTGGAG	623
Qy	101	ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu	120
Db	624	AGGGCAGCCAGCCGAGCAACTGTGCGCAGCTTCCACCATTGAAGATCTTTTGGAAAGA	683
Qy	121	LeuProGluThrSerSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro	140
Db	684	CTACCAAGACGAGTGGGAAACCAACCCGAGATCTCTTTTAATTTTAAGTTCTATCCCC	743
Qy	141	ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla	160
Db	744	ACGAGGAGTTTATCACTTCAGCAGAGCTTCAGGTTTCCGGAACAGATGCAAGATGCT	803
Qy	161	LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleLysProAla	180
Db	804	TTAGGAACAATAGCAGTTCCATCAGCGAATTAATTTATGAATCATAAACCTGCA	863
Qy	181	ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn	200
Db	864	ACGCCAACTCGAAATTTCCCGTGACACAGATTTTGGACACAGGTTGGTGAATCAGAA	923
Qy	201	AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly	220
Db	924	GCAAGCAGTGGGAAAGTTTGTATGTACCCCCCGCTGTGATCGCGTGGACTGACAGGGA	983

Qy	221	HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer	240
Db	984	CAGCCCAACCATGGATTCTGGTGGAGTGGCCACTTGGAGGAGAAACAAGGTGTCTCC	1043
Qy	241	LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle	260
Db	1044	AAGAGACATGTTAGATTAAGCAGTCTTTGACCAGATGAACACACTGTGTACAGATA	1103
Qy	261	ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu	280
Db	1104	AGGCCATTGCTAGTAACCTTTTGCCCATGATGGAAAAGGGCATCTCTCCACAAAGAGAA	1163
Qy	281	LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro	300
Db	1164	AAACGTCACGCCAACCAACAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAAGAGACCCCT	1223
Qy	301	LeuTyrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyr	320
Db	1224	TTGTACGTGGACTTCAGTGACGTGGGTGGAATGACTGGATTGTGGCTCCCCGGGGTAT	1283
Qy	321	HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr	340
Db	1284	CAGCCCTTTTACTGCCAGCGAGAAATGCCCTTTCTCTGGCTGATCATCTGNACTCCACT	1343
Qy	341	AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys	360
Db	1344	AATCATGCCATTGTTCAAGCGTTGGTCAACTCTGTTAACTCTAAGATTCCTAAGGCATGC	1403
Qy	361	CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal	380
Db	1404	TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTACGAGAAATGAAGGTT	1463
Qy	381	ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg	396
Db	1464	GTATTAAGAAGTAATCAGGACATGTTGTGGAGGGTTGTGGGTGTGCGTGC	1511
RESULT 4			
ID	AAV01679	standard; cDNA; 1547 BP.	
XX	AAV01679;		
XX	25-MAR-2003 (revised)		
DT	27-MAR-1998 (first entry)		
XX	Bone morphogenetic protein BMP-2 encoding DNA.		
DE	Bone morphogenetic protein; BMP; growth; vitamin D; fracture; arthritis;		
KW	surgical lesion; periodontal disease; osteoporosis; rickets; db.		
XX	Unidentified.		
XX	OS		
XX	US5693615-A.		
XX	02-DEC-1997.		
XX	23-JAN-1995; 95US-00377292.		
XX	05-JUN-1991; 91US-00709621.		
PR	27-MAR-1992; 92US-00856110.		
PR	09-DEC-1992; 92US-00988363.		
PR	07-SEP-1993; 93US-00117367.		
PR	13-MAY-1994; 94US-00243435.		
XX	(PROC) PROCTER & GAMBLE CO.		
XX	Stone RL;		
XX	WPI; 1998-031789/03.		
XX	Generation of new bone growth - by co-administering bone morphogenetic		
PT	protein and vitamin D.		

XX Claim 1; Col 19-22; 18pp; English.
 XX A new method has been developed for generating new bone growth in a
 CC mammal. The method comprises administering a bone morphogenetic protein
 CC in combination with a vitamin D compound, where: (a) the bone
 CC morphogenetic protein is BMP-2 and is administered in an amount of 500-
 CC 1000 ng in combination with about 6 ng vitamin D compound; or (b) the
 CC bone morphogenetic protein is BMP-4 and is administered in an amount of
 CC about 62.5 ng in combination with about 6 ng vitamin D compound. The
 CC present sequence encodes BMP-2. The method is used for treating bone
 CC defects or disorders, e.g. fractures, surgical lesions, periodontal
 CC disease, osteoporosis, arthritis and rickets. (Updated on 25-MAR-2003 to
 CC correct PF field.)
 XX SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.2e-174 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-801-648-2 (1-396) x AAV01679 (1-1547)

QY 1 MetValAlaGlyThrArgCysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuGly 20
 DB 324 ATGGTGGCGGACCGCTGCTTCTAGCGTTGCTGCTCCCGCAGGTCTCTCGGCGGC 383
 QY 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaSerSerGlyVal 40
 DB 384 GCGGCTGGCTGCTCCGAGCTGGCGCCGACGAGTTCCGCGCGCGCTGCTGGCGCGC 443
 QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuLeuLeuSerMet 60
 DB 444 CCTCATCCAGCCCTCTGACGAGGTCTGAGCGAGTTGCGAGTTCGCGCTGCTCAGCATG 503
 QY 61 PheGlyLeuLeuGlnArgProThrProSerArgAspAlaValValProProThrMetLeu 80
 DB 504 TTCCGCTGAAACAGAGACCCACCCCGCAGCGAGCGCGTGGTGGTGGTGGTGGTGG 563
 QY 81 AspLeuTyArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 DB 564 GACCTGTATCGAGGACCTCAGTTCAGCGCGGCTACCCCGCCCGACACCCCGTTGAG 623
 QY 101 ArgAlaAlaSerArgAlaAlaSerThrValArgSerPheHisGluGluSerLeuGlu 120
 DB 624 AGGCGAGCCAGCGGACCAACTGTGCGCAGCTTCCACCATGAGATCTTTGGAGAA 683
 QY 121 LeuProGluThrSerGlyThrThrArgArgPhePheAsnLeuSerSerIlePro 140
 DB 684 CTACCAAGAACAGTGGGAAACACACCGGAGATTCTTCTTAATTTAAGTTCTATCC 743
 QY 141 ThrGluGluPheThrSerAlaGluLeuGlnValPheArgGluMetGlnAspAla 160
 DB 744 ACGGAGGAGTTATACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 803
 QY 161 LeuGlyAsnAsnSerSerPheHisHisArgGlyLeuLeuLeuLeuLeuLeuLeu 180
 DB 804 TTAGGAACAACATAGCAGTTCCATCACCAGCAATTAATTTATGAATCATAAACCTGCA 863
 QY 181 ThrAlaAsnSerIysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 DB 864 ACAGCCAACTCGAAATTCGCGGTGACAGACTTTTGGACACAGGTTGGTGAATCAGAT 923
 QY 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrIleGlnGly 220
 DB 924 GCAAGCAGTGGGAAAGTTTGTATGTACCCCGCTGTGATCGGTGGAGCTCAGCAGGGA 983
 QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluGluGlnGlyValSer 240

DB 984 CACGCCAACCATGGATTCTGGTGGAGTGGCCCACTTTGGAGGAGAAACAAGGTGTCTCC 1043
 QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 DB 1044 AAGAGACATGTTAGGATAAGCAGGTCTTTGCCAACAGATGACACACAGCTGGTGCACAGATA 1103
 QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisGlySerGlu 280
 DB 1104 AGGCCATTGCTAGTAACCTTTTGGCCATCATGGAAGAGGCGCATCTCTCCACAAAAGAGAA 1163
 QY 281 LysArgGlnAlaLysHisGlyGlnArgLysArgLeuLysSerSerCysIysArgHisPro 300
 DB 1164 AAACGTCAGGCCAAACACAAACACAGCGGAAACGCTTAAGTCCAGCTGTAAGAGACACCC 1223
 QY 301 LeuTyValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTy 320
 DB 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGATGACTGCTGCTGGCTCCCGCGGGTAT 1283
 QY 321 HisAlaPheTyrcysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 DB 1284 CAGCCCTTTTACTGCCACGAGAGATGCCCTTTTCTCTGGCTGATCATCTGAACCTCACT 1343
 QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProIysAlaCys 360
 DB 1344 AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTAACTCTTAAGATTCTTAAGGCGATGC 1403
 QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyLeuAspGluAsnGluLysVal 380
 DB 1404 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGATGAAGAGTT 1463
 QY 381 ValLeuLysAsnTyrcysGlnAspMetValValGluGlyCysGlyCysArg 396
 DB 1464 GTATTAAAGAACTATCAGACATGTTGTGGAGGGTGTGGGTGTGCG 1511
 RESULT 5
 ABK90308
 ID ABK90308 standard; DNA; 1547 BP.
 XX AC ABK90308;
 XX 21-OCT-2002 (first entry)
 XX DE DNA encoding human bone morphogenetic protein 2 (BMP2).
 XX KW Bone morphogenetic protein 2; BMP2; cancer; breast cancer; lung cancer;
 XX KW Gene; ss; human.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX CDS 324..1514
 FT /*tag= a
 FT /product= "BMP2 protein"
 FT 429..1127
 FT /*tag= b
 FT /note= "TGF-beta propeptide"
 FT replace(432,G)
 FT /*tag= c
 FT /standard name= "Single nucleotide polymorphism"
 FT replace(584,G)
 FT /*tag= d
 FT /standard name= "Single nucleotide polymorphism"
 FT replace(893,A)
 FT /*tag= e
 FT /standard name= "Single nucleotide polymorphism"
 FT 1209..1511
 FT /*tag= f
 FT /note= "TGF-beta-like domain"
 XX WO200254940-A2.
 XX 18-JUL-2002.
 XX

PF 11-JAN-2002; 2002WO-US000610.
 XX
 PR 12-JAN-2001; 2001US-0261252P.
 XX
 PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
 XX
 PI Langenfeld J;
 XX
 DR WPI; 2002-575416/61.
 XX
 PT Treating cancer, e.g. lung cancer, comprises administering a bone
 PT morphogenic protein-2 (BMP-2) activity inhibitor, or a vector encoding
 PT the inhibitor or an antisense oligonucleotide that binds to a BMP-2
 PT nucleic acid sequence.
 XX
 PS Disclosure; Page 37-40; 162pp; English.
 XX
 CC This invention relates to a novel method for treating cancer comprising
 CC administering to a patient a bone morphogenic protein-2 (BMP-2) activity
 CC inhibitor or an expression vector which has a nucleic acid sequence
 CC encoding the BMP-2 activity inhibitor or which encodes an antisense
 CC oligonucleotide that binds to a BMP-2 nucleic acid sequence. Inhibitors
 CC of BMP-2 activity encompassed in the invention are the proteins noggin,
 CC chordin gremlin, cerberus 1 homologue and DAN. The method of the
 CC invention which utilises a BMP-2 activity inhibitor or an expression
 CC vector, is useful in diagnosing or treating cancers such as breast cancer
 CC or lung cancer. A kit is useful in the administration of the BMP-2
 CC activity inhibitor in the treatment of cancers. The present sequence
 CC represents the DNA encoding the human bone morphogenetic protein (BMP2)
 CC protein used in the method of the invention
 XX
 SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6.2e-174 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x ABK90308 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
 Db ATGTGGCCGGAGCCCGCTGCTTCTAGCGTGTCTTCCCGAGGTCCTCTCGGGCGGC 383
 Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
 Db CGGCTGGCTCGTTCGGAGCTGGGCCGAGGAGTTCCGGCGCGCGTCTCGGGCGGC 443
 Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
 Db CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTCCGAGTTCCGCTGCTCAGCATG 503
 Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
 Db TTCGGCTTGAACAGAGACCCACCCCGAGGAGCGCGTGGTCCCGCCCTACATGCTA 563
 Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db GACTGTATCGAGGCATCTAGGTGAGCCGGGCTCACCCGCCCCAGACACCGGTTGGAG 623
 Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
 Db AGGGCAGCCAGCCGAGCCACACCTGTGGCAGCTTCCACCATGAAGAATCTTTGGAAGA 683
 Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
 Db CTACAGAAACGAGTGGGAAACCAACCCGGAGATTCCTTTTAATTTAAGTTTCATCCCC 743
 Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160

744 ACGGAGGAGTTTATCACTCTCAGCAGAGCTTTCAGGTTTTCCGAGAACAGATGCAAGTGCT 803
 Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
 Db TTAGGAACAATAGCAGTTTCCATCACCGAATTAATATTTATGAATCATAAAAACCTGCA 863
 Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 Db ACAGCCAACTCGAAATTTCCCGTGACCGAGCTTTTGACACACCGAGTTGGTGAATCAGAT 923
 Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
 Db GCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGTATCGGTGAGTGCACAGGGA 983
 Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
 Db CACGCCAACCATGATTCGTGTGTGTAAGTGGCCACTTTCGAGGAGAAACAAGGTGTCTCC 1043
 Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
 Db AAGAGACATGTTAGGATAAGCAGGTCTTTGCACCAAGATGAACACAGCTGTGTACAGATA 1103
 Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db AGGCCATTGCTAGTAACCTTTTGCCCATGATGGAAGAGGCATCTCTCCACAAAAGAGAA 1163
 Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 Db AAACGTCAAGCCAAACACAAACACGCGAAACGCTTAAGTCCAGCTGTAAAGAGACACCT 1223
 Qy 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyr 320
 Db TTGTACGTGGACTTCAGTGACGTGGGTGGAATGAGTGGATTTGGTCTCCCGGGGTAT 1283
 Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db CACGCTTTTACTGCCACGAGGAATGCCCTTTCTCTGCTGATCATCTGAACTCCACT 1343
 Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 Db AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTTAACTCTAAGATTCTTAAGGCATGC 1403
 Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 Db TGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAATGAAAAGTT 1463
 Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 Db GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTCTCC 1511

RESULT 6
 ABX76358
 ID ABX76358 standard; DNA; 1547 BP.
 XX
 AC ABX76358;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Lung cancer-associated polynucleotide #222.
 XX
 KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; arelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 OS Unidentified.
 XX
 FN WO200286443-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012476.

XX 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350668P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX AZIZ N, Murray R;
 PI
 XX WPI; 2003-093161/08.
 DR P-PSDB; ABU56629.
 XX
 PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.
 XX
 PS Claim 22; Page 357; 453pp; English.
 XX
 CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridizes
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersecretory pneumonia, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
 CC invention
 XX
 SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6.2e-174 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-801-648-2 (1-396) x ABX76358 (1-1547)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
 DB 324 ATGGTGGCGGACCGCGTGTCTTCTAGGTGCTGCTTCCAGGTCTCTCTGGCGCGC 383
 QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
 DB 384 GCGGCTGGCGCTGTTCCGAGCTGGCGCGCAGAAAGTTCCGCGCGCGCTCGTGGCGCGC 443
 QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 DB 444 CCTCATCCACCGCTCTGACGAGGTCTGACGAGTTCGAGTTCGCGCTGCTCAGCATG 503
 QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
 DB 504 TTCGGCTGGAACAGAGACCCACCCAGAGGCGCGGTGTGCTGCCCTTACATGTCTA 563
 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 DB 564 GACCTGTATCGCAGGACCTCAGGTTCAGCGCGGCTCACCGCGCCACAGACCACCGGTTGGAG 623

QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
 DB 624 AGGCGAGCCAGCCGAGCCACACTGTGGCAGCTTCCACCATGAAGATCTTTGGAGAA 683
 QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
 DB 684 CTACCAGAAACGAGTGGGAAAAACAACCGGAGATTCTCTTTAAATTTAAGTTCTATCC 743
 QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGluAspAla 160
 DB 744 ACGGAGGAGTTTATCACCCTCAGCAGAGCTTCCAGGTTTCCGAGAACACATGCAAGAT 803
 QY 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAla 180
 DB 804 TTAGAAACATAGCAGTTTCCATCCGAAATTAATTAATTAATTAATTAATTAATTAAT 863
 QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 DB 864 ACAGCAACTCGAAATTCCTCGTGCACAGACTTTTGGACACACAGGTTGGTGAATCAGA 923
 QY 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
 DB 924 GCAAGCAGGTGGAAAGTTTGTATGTACCCCTGATGCGGTGGACTGCACAGGGA 983
 QY 221 HisAlaAsnHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
 DB 984 CACGCCAACCATGATTCGTGTGGAGTGGCCACTTGGAGGAGAAACAGGTGTCTCC 1043
 QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 DB 1044 AAGAGACATGTTAGCATAAAGCAGGTCTTTGCAACAAGATGAACACAGCTGGTGCAGATA 1103
 QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 DB 1104 AGGCCATGTGTAGTAACCTTTTGGCCATGATGAAAGAGGCGCATCTCTCCACAAAGAGA 1163
 QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 DB 1164 AAGCTCAGCCAAACACACACAGCGGNAAGCCTTAAAGTCCAGCTGTAAAGAGACACCT 1223
 QY 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTrpIleValAlaProProGlyTyr 320
 DB 1224 TTGTACGTGGACTTTCAGTGACGTGGGTGGAAATGACTGGATTGTGGCTCCCGGGGTAT 1283
 QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 DB 1284 CACGCTTTTACTGCCAGGAGATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT 1343
 QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 DB 1344 AATCATGCCATTTGTTTCAGACGTTGGTCAACTCTGTAACTCTTAAGATTCTTAAGCATGC 1403
 QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 DB 1404 TGTGTCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGCAGAGATGAAGGTT 1463
 QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 DB 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGTCG 1511

RESULT 7

ACF34481
 ID ACF34481 standard; DNA; 1547 BP.

AC ACF34481;

DT 15-OCT-2003 (first entry)

DE Gene encoding angiogenesis protein BNO99.

XX Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antipsoriatic; antiarteriosclerotic; cardiant; vasotropic; angiogenesis;

gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis; diabetic retinopathy; cardiovascular disease; atherosclerosis; ischemic limb disease; coronary artery disease; gene; ds.

Homo sapiens.

WO2003027285-A1.

03-APR-2003.

19-SEP-2002: 2002WO-AU001282.

27-SEP-2001: 2001AU-00007973.

27-SEP-2001; 2001AU-00007974.
11-OCT-2001: 2001AU-00008310

29-OCT-2001; 2001AU-00008532.

28-AUG-2002; 2002AU-00951032.

(BION-) BIONOMICS LTD.

Gamble JR, Hahn CN, Vadas M

WPI; 2003-354655/33.

• 00740YCW / 0003-3

New allylogenic yellows
prognosticating or t

cancer, rheumatoid cardiovascular di

Claim 2: SEO ID NO 36: 90pp: English.

The invention relates to the isolation

encoding proteins (ABR64180-ABR6428) involved in the process of angiogenesis. The nucleic acid molecules are useful in identifying and/or obtaining full-length human genes involved in an angiogenic process. The nucleic acid molecule, polypeptides or complexes encoded, cells or genetically modified non-human animals derived from these are useful for the screening of candidate pharmaceutical compounds used in treating angiogenesis-related disorders. They are also useful for diagnosing, prognosticating or treating an angiogenesis-related disorder, which involves uncontrolled or enhanced angiogenesis or is a disorder in which a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or cardiovascular diseases such as atherosclerosis), or involves inappropriately arrested or decreased angiogenesis or is a disorder in which an expanding vasculature is of benefit (e.g. ischemic limb disease or coronary artery disease). The modulator of expression or activity of the polypeptide encoded by the nucleic acid sequence is useful for manufacturing a medicament for the treatment of an angiogenesis-related disorder. This sequence corresponds to the gene encoding one of the novel angiogenic protein

Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Instrument Scores:

Document Scores:					
Seq. No.:	6.2e-174	Length:	1547		
Score:	2098.00	Matches:	396		
Percent Similarity:	100.00%	Conservative:	0		
Local Similarity:	100.00%	Mismatches:	0		
Global Similarity:	100.00%	Indels:	0		
Gap Match:	8	Gaps:	0		

0-801-648-2 (1-396) x ACP34481 (1-1547)

1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20

324 ATGGTGGCCGGGACCCGGTGTCTTCTA GGGTGGTGGTCCCA GGTCTCTGGGGGGC 383

21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40

384 GCGGCTGGCCTCGTTCCGGAGCTGGGC CGCAGGAAGTTCGGCGGGCGTGGTGGGCGGC 443

RESULT 8

ACF05920
 ID ACF05920 standard; cDNA; 1547 BP.
 AC ACF05920;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human bone morphogenic protein 2A polynucleotide.
 XX
 KW Bone morphogenic protein 2A; BMP-2A; human; glaucoma; diagnosis; therapy;
 KW ophthalmological; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 324..1514
 FT /*tag= a
 FT /product= "BMP-2A"
 XX
 PN WO2003055443-A2.
 XX
 PD 10-JUL-2003.
 XX
 PF 31-OCT-2002; 2002WO-US035251.
 XX
 PR 31-OCT-2001; 2001US-0334852P.
 XX
 PA (ALCO-) ALCON INC.
 PA (UYNT-) UNIV NORTH TEXAS HEALTH SCI CENT.
 XX
 PI Clark AF, Wordinger RJ;
 XX
 DR WPI: 2003-559253/52.
 DR P-PSDB; ABR62824.
 XX
 PT Diagnosing glaucoma in a sample comprises detecting altered expression of
 PT bone morphogenic proteins in sample from a cell or bodily fluid.
 XX
 PS Claim 1; Fig 1a-c; 55pp; English.
 XX
 CC The present sequence is a nucleotide sequence for human bone morphogenic
 CC protein 2A (BMP-2A). RT-PCR showed BMP-2 to be expressed in the human
 CC trabecular meshwork and optic nerve head. A claimed method for diagnosing
 CC glaucoma involves detecting altered expression of a BMP family member
 CC such as BMP-2A by PCR in a sample obtained e.g. from blood or buccal
 CC cells. Primers used in the PCR may comprise contiguous nucleotides of the
 CC present sequence. A claimed method for treating glaucoma comprises
 CC administering an agonist of BMP-2, BMP-4, BMP-5, BMP-7 or Smad 1/5, or an
 CC antagonist of chordin, gremlin or follistatin. A claimed method of
 CC identifying a therapeutic agent for treatment of glaucoma comprises
 CC identifying a substance that inhibits or stimulates BMP-induced Smad
 CC signalling pathways or BMP-regulated gene expression, using recombinant
 CC cells expressing BMP-2A, BMP-4, BMP-5 or BMP-7
 XX
 SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.2e-174 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-10-801-648-2 (1-396) x ACF05920 (1-1547)
 QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
 DB 324 ATGGGCGCGGACCGCGCTCTCTTAGCGTTGCTCTCCAGGTCTCTCTGGCGGC 383
 QY 21 AlaAlaGlyLeuValProGlnLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
 DB 384 GCGGCTGGCTCTGTTCCGGAGCTGGGCGCGAGAGTTCCGCGCGCGCTCTCTGGCGCGC 443

QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 DB 444 CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTGAGTTGGGCTGCTCAGCATG 503
 QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
 DB 504 TTGGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGGTGGTGGTGGTGGTGGT 563
 QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 DB 564 GACCTGTATCGAGGCACTCAGGTGAGCGCGGCTCACCCGCGCCAGACACCGGTTGGAG 623
 QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
 DB 624 AGGCGAGCCAGCCAGCCCAACACTGTGCGGAGCTTCCACCATGAAGATCTTTGGAAGAA 683
 QY 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
 DB 684 CTACCAGAAACGAGTGGGAAACACCCGAGATTTCTTTTAAATTTAAGTTCTATCCCC 743
 QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 DB 744 ACGGAGGAGTTTATCACCCTCAGCAGAGCTTCCAGGTTTCCGAGAACACATGCAAGATGCT 803
 QY 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAla 180
 DB 804 TTAGGAACAATAGCAGTTTCATCACCAGATTAATTAATTAATTAATTAATTAATTAATTA 863
 QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 DB 864 ACAGCCAACTCGAAATTCCTCCGTCACACAGACTTTTGGACACAGGTTGGTGAATCAGAAT 923
 QY 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
 DB 924 GCAAGCAGTGGGAAAGTTTGTATGTACCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 983
 QY 221 HisAlaAsnHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
 DB 984 CACGCCAACCATGGATTCGTGTGGAGTGGCCACTTTGGAGAGAAACAGGTGTCTCTCC 1043
 QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
 DB 1044 AAGAGACATGTTAGGTAAGCAGGTCTTTGCAACCAAGATGAACACAGCTGTGTGTGTGTGT 1103
 QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 DB 1104 AGGCCATTGCTAGTAACCTTTTGGCCATGATGAAAGAGGCGATCTCTCCACAAAAGAGAA 1163
 QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 DB 1164 AAACGTCAAGCCAAACACAAACAGCGGAAACGCTTAACTTAACTTAACTTAACTTAACTTAA 1223
 QY 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTyrIleValAlaProProGlyTyr 320
 DB 1224 TTGTAGTGGACTTCAGTGACGTGGGTGGAATGATGATGATGATGATGATGATGATGATGATG 1283
 QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 DB 1284 CACGCTTTTACTGCGCAGGAAATGCGCTTTTCTCTGCGCTGATCATCTGTAACCTTCAACT 1343
 QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 DB 1344 AATCATGCCATTGTTGACAGCTTGGTCACTCTGTTAACTCTTAAGTTCTTAAGGCGATGC 1403
 QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 DB 1404 TGTGTCCGACAGAACTCAGTGCTATCTCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1463
 QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 DB 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGTGTGTGTGTGTGTGTGT 1511

RESULT 9	DB:	10	Gaps:	0
ADD14609	US-10-801-648-2 (1-396) x ADD14609 (1-1547)			
ID	ADD14609 standard; cDNA; 1547 BP.			
XX	AC			
XX	AC			
XX	XX			
XX	DT			
XX	01-JAN-2004 (first entry)			
XX	Human src biomarker polynucleotide SEQ ID NO:3.			
DE				
XX	predictor set; protein tyrosine kinase activity modulator;			
XX	protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;			
KW	gene therapy; drug sensitivity; genetic profile; cancer; human; gene; ss.			
KW				
XX	OS			
XX	Homo sapiens.			
XX	WO2003062395-A2.			
FN				
XX	31-JUL-2003.			
PD				
XX	17-JAN-2003; 2003WO-US001981.			
PF				
XX	18-JAN-2002; 2002US-0350061P.			
PR				
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.			
XX	PA			
XX	Huang F, Fairchild CR, Lee FY, Shaw P;			
FI				
XX	WPI; 2003-636735/60.			
DR	P-PSDB; ADD14015.			
XX				
XX	New polynucleotides and polypeptides for predicting the activity of			
PT	compounds that interact with protein tyrosine kinases and/or protein			
PT	tyrosine kinase pathways.			
XX				
PS	Claim 2; SEQ ID NO 3; 139pp; English.			
XX				
CC	The present invention describes a predictor set comprising a plurality of			
CC	polynucleotides or polypeptides whose expression pattern is predictive of			
CC	the response of cells to treatment with a compound that modulates protein			
CC	tyrosine kinase activity or members of the protein tyrosine kinase			
CC	pathway. Also described: (1) predicting whether a compound is capable of			
CC	modulating the activity of cells, comprising obtaining a sample of cells,			
CC	determining whether the cells express a plurality of markers, and			
CC	correlating the expression of the markers to the compound's ability to			
CC	modulate the activity of the cells; (2) a plurality of cell lines for			
CC	identifying polynucleotides and polypeptides whose expression levels			
CC	correlate with compound sensitivity or resistance of cells associated			
CC	with a disease state; and (3) identifying polynucleotides and			
CC	polypeptides that predict compound sensitivity or resistance of cells			
CC	associated with a disease state, comprising subjecting the plurality of			
CC	cell lines to one or more compounds, analysing the expression pattern of			
CC	a microarray of polynucleotides or polypeptides, and selecting or			
CC	polynucleotides or polypeptides that predict the sensitivity or			
CC	resistance of cells associated with a disease state by using the			
CC	expression pattern of the microarray. The polynucleotides and			
CC	polypeptides have cytostatic activities, and can be used in gene therapy.			
CC	The polynucleotides and polypeptides are useful in predicting the			
CC	activity of compounds that interact with protein tyrosine kinases and/or			
CC	protein tyrosine kinase pathways. These may be used in determining drug			
CC	sensitivity in patients to allow the development of individualized			
CC	genetic profiles which aid in treating diseases and disorders (e.g.			
CC	cancer) based on patient response at a molecular level. The present			
CC	sequence is used in the exemplification of the present invention.			
XX				
SQ	Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;			
Alignment Scores:				
Pred. No.:	6.2e-174	Length:	1547	
Score:	2098.00	Matches:	396	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	

Db 1344 AATCATGCCATTGTTTCAGACGCTGGTCAACTCTGTAACTCTAAGGATCTTAAGGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluVal 380
Db 1404 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAGAAGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGluCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGACATGTTGTGTGGAGGGTTGTGGGTGTCG 1511

RESULT 10

ID ADE85186
AD85186 standard; DNA; 1547 BP.

XX AC ADE85186;

DT 29-JAN-2004 (first entry)

DE Farnesyl transferase inhibitor modulated leukemia associated gene #405.

XX ss; cytostatic; farnesyl transferase inhibitor; gene expression;
KW quinolone; leukemia; cancer.

XX OS Homo sapiens.

XX FN WO2003038129-A2.

XX PD 08-MAY-2003.

XX PF 30-OCT-2002; 2002WO-US034784.

XX PR 30-OCT-2001; 2001US-0338997P.

XX PR 30-OCT-2001; 2001US-0340081P.

XX PR 30-OCT-2001; 2001US-0340938P.

XX PR 30-OCT-2001; 2001US-0341012P.

XX PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

XX PI Raponi M;

XX DR WPI; 2003-513497/48.

XX PT Determining whether a patient will respond to treatment with a farnesyl

PT transferase inhibitor, by analyzing the expression of gene that is

PT differentially modulated in the presence of the inhibitor.

XX PS Disclosure; SEQ ID NO 405; 346pp; English.

CC The invention relates to a method of determining whether a patient will
CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
CC analyzing the expression of gene that is differentially modulated in the
CC presence of an FTI. The method is useful for determining whether a
CC patient will respond to treatment with a FTI such as (B)-6-famino(4-
CC chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl)-4-(3-chlorophenyl)-1-
CC methyl-2-(1H)quinoline, monitoring the therapy of a patient, treating a
CC patient with leukemia with FTI if the analysis indicates that the patient
CC will respond. This sequence corresponds to a gene whose expression may be
CC modulated in the presence of FTI.

XX SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.2e-174	Length:	1547
Score:	2098.00	Matches:	396
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-801-648-2 (1-396) x ADE85186 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20

Db 324 ATGGTGGCCGGGACCCCGCTGTCTTCTAGCGTTGCTGTCCCGAGGTCTCTCTGGCGCGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgGlyPheAlaAlaAlaSerSerGlyVal 40
Db 384 GCGGTGCGCTCGTTCGGAGCTGGGCGCGAGGAGTTTCGGCGCGCGCTGTCTGGCGCGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCCAGCCCTCTGACGAGGTCTGAGCGAGTTGAGTTGCGGTGCTGTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 504 TTCGCGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGTGTCCCGCTTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGAGGCACTCAGGTGAGCCGGGCTCACCGGCCAGACCCCGGTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGlu 120
Db 624 AGGCGAGCCAGCCGCGCCAACTGTGCGCAGCTTCCACCATGAAGATCTTTGGAGAA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCAGAAACGAGTGGGAAACAAACCGGAGATCTTCTTTAATTTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGluMetGlnPheAla 160
Db 744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTTCAGGTTTTCCGAGAAACAGATGCAATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 804 TTAGGAAACAAATAGCAGTTTCACTCAGCAATTAATTAATTAATTAATTAATTAATTA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACTCGAAATTCCTCCGTGACAGACTTTTGGACACCCAGCTTGTGTGAATCAGAAT 923
Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrIleGly 220
Db 924 GCAAGCAGTGGGAAAGTTTGTATGTACCCCGCTGTGTGCGGTGGAGTGCACAGGGA 983
Qy 221 HisAlaAsnHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CAGCCAAACCATGGATTCTGTGTGAAGTGGCCCACTTGGAGAGAAACAGAGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGAGACATGTAGGATAAGCAGGCTTTTCACCAAGATGAACACAGCTGGTCACAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGAAGGCGCATCTCTCCACAAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisGlyGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTGAAGACACCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGATGACTGGATTGTGGCTCCCGCGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCGCTTTTACTGCGCAGGAGATGCCCTTTTCTCTGGCTGATCATCTGAACCTCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 AATCATGCCATTGTTTCAGACGTTGTCACCTCTGTAACTCTTAAGATTCCTAAGGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluVal 380

Db 1404 TGTGTCGACAGAACTCAGTGTCTATCTCGATCTGTACCTTGACGAGATGAAAGGTT 1463

Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
|||||
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTCGC 1511

RESULT 11
AAD63420
ID AAD63420 standard; DNA; 1547 BP.
XX
AC AAD63420;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human bone morphogenetic protein (BMP)-2 DNA.
XX
KW Human; BMP; bone morphogenetic protein; cancer; therapy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 324..1514
FT /*tag= a
FT /product= "Human BMP-2 protein"
FT sig_peptide 324..1169
FT /*tag= b
FT /label= Signal_peptide
FT misc_feature 429..1127
FT /*tag= d
FT /note= "Transforming growth factor (TGF)-beta propeptide
FT region"
FT replace(432,G)
FT /*tag= e
FT replace(584,G)
FT /*tag= f
FT replace(893,T)
FT /*tag= g
FT mat_peptide 1170..1511
FT /*tag= c
FT /product= "Mature human BMP-2 protein"
FT 1209..1511
FT /*tag= h
FT /note= "Transforming growth factor (TGF)-beta-like
FT domain"
XX
PN US2003134790-A1.
XX
XX 17-JUL-2003.
XX
XX 02-MAY-2002; 2002US-00139814.
XX
XX 11-JAN-2002; 2002US-00044716.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
XX Langenfeld J;
XX
XX WPI; 2003-829645/77.
DR P-PSDB; ABW01849.
XX
PT Treating cancer, e.g. carcinoma of the breast, bladder, colon, kidney,
FT lung, ovary, thyroid, endometrium, omental, testis or liver, comprises
FT administering to the patient a bone morphogenetic protein-4 activity
FT inhibitor.
XX
XX Disclosure; Page 15-17; 64pp; English.
XX
XX The present invention relates to the use of BMP (bone morphogenetic
CC protein)-2 and BMP-4 used in treating cancer. The invention is useful for
CC treating cancer, e.g. carcinoma of the breast, bladder, colon, lung,
CC kidney, ovary, thyroid, endometrium, omental, testis and liver. The
CC present sequence is human bone morphogenetic protein (BMP)-2 DNA
XX

SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.2e-174 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-801-648-2 (1-396) x AAD63420 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
|||||
Db 324 ATGTGGCCGGAGCCCGTGTCTTAGCGGTGCTCTTCCCAAGGTCCTCTCGGGCGGC 383

Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLaserSerArg 40
|||||
Db 384 GGGCTGGCTCGTTCGGAGCTGGCCCGCAGAGTTTCGGGGGGCGTCTCGGGCGGC 443

Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
|||||
Db 444 CCTCATCCAGCCCTCTGACGAGTCTCTGAGCGAGTTCCGAGTTTCGGCTGCTCAGCATG 503

Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
|||||
Db 504 TTCGGCTGAACAACAGAGACCCACCCCGCAGGAGCCCGTGGTGGCCCTTACATGCTA 563

Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
|||||
Db 564 GACCTGTATCGAGGCACTCAGTCCAGCGGGTCCACCCGCCAGACACCGGTTGGAG 623

Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
|||||
Db 624 AGGCGAGCCAGCCGAGCAACACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAAGAA 683

Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
|||||
Db 684 CTACCAGAAACGAGTGGGAAACAACCCGAGATCTCTTTAATTTAAGTTCTATCCCC 743

Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
|||||
Db 744 ACGGAGGAGTTTATCACCCTCAGCAGAGCTTCAGGTTTTCGAGBACAGATGCAAGTGCT 803

Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleLysProAla 180
|||||
Db 804 TTAGGAAACAATAGCAGTTCCATCACCGAATTAATATTATGAAATCATAAAACTGCA 863

Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
|||||
Db 864 ACAGCCAACTCGAAATTCGCCGTGACCAAGCTTTTGACACCAAGTTGGTGAATCAGAT 923

Qy 201 AlaserArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
|||||
Db 924 GCAGCAGGTGGGANAAGTTTGTATGTACCCCGCTGTGTGATGGTGGATGTCACAGGA 983

Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluLysGlnGlyValSer 240
|||||
Db 984 CAGCCCAACCATGATTCGTGGTGGAGTGGCCACTTGAGGAGAGAAACAAGGTGTCTCC 1043

Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGluIle 260
|||||
Db 1044 AAGAGACATTTAGGATAAGCAGTCTTTTGACCAAGATGAACACAGCTGTCTCAGATA 1103

Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
|||||
Db 1104 AGGCCATTGTAGTAACCTTTTGCCCATGATGGAAGGGCATCTCTCTCCANAAAGAGAA 1163

Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
|||||
Db 1164 AAAGTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAAGAGACACCT 1223

Qy 301 LeuTyrValAspPheSerAspValGlyTyrPasnAspTrpIleValAlaProProGlyTyr 320
|||||

Db 1224 TTGTACGTGGACTTCAGTGCACGTGGGTGGATGACTGGATTGTGGCTCCCGGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCCCTTTACTGCGCAGGAGAAAGCCCTTTCTCTGCTGTGATCATCTGAACCTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 AATCATGCCATTGTTTCAGACGGTTGCTCAACTCTGTTAACTCTAAGATTCTTAAGSCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACTTTCAGCAGAAATGAAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGluAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGACATGTTGTGGAGGTTGTGGGTGTCGC 1511
RESULT 12
ABT17041
ID ABT17041 standard; DNA; 1547 BP.
XX AC ABT17041;
XX DT 03-APR-2003 (first entry)
XX DE Human MP21 gene BWP2 SEQ ID No 15.
XX KW Cytostatic; p21 pathway modulating agent; cancer; angiogenic; apoptotic;
KW cell proliferation disorder; MP21; gene; ds.
XX OS Homo sapiens.
XX PN WO2003006990-A1.
XX PD 23-JAN-2003.
XX PP 10-JUL-2002; 2002WO-US021549.
XX PR 12-JUL-2001; 2001US-0305017P.
PR 10-OCT-2001; 2001US-0328491P.
PR 15-FEB-2002; 2002US-0357452P.
XX PA (EXEL-) EXELIXIS INC.
XX PI Friedman L, Plowman GD, Belvin M, Li D, Funke RP;
XX DR P-PSDB; ABJ19767.
XX PT Identifying candidate p21 pathway modulator, by contacting an assay
PT system having modifiers of p21 polypeptide or gene with a test agent to
PT provide a reference activity in system and detecting test agent-biased
PT activity.
XX PS Example; Page 86-87; 199pp; English.
XX CC The invention relates to a novel method for identifying a candidate p21
CC pathway modulating agent. The novel method comprises contacting an assay
CC system, comprising a purified MP21 polypeptide (modifier of p21) or
CC nucleic acid, with a test agent under conditions, so that but for the
CC presence of a test agent, the assay system provides a reference activity
CC and detection of test agent-biased activity of the assay system. The
CC novel method of the invention is useful for identifying a candidate p21
CC pathway modulating agent. The invention also includes a method for
CC modulating the p21 pathway of a cell, and a method for diagnosing a
CC disease e.g. cancer in a patient. The identified modulators are useful in
CC diagnosis, therapy and pharmaceutical development. The modulators are
CC useful in a variety of diagnostic and therapeutic applications including
CC angiogenic, apoptotic and cell proliferation disorders. This
CC polynucleotide sequence represents a gene encoding an MP21 protein of the
CC invention

XX SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6.2e-174 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-801-648-2 (1-396) x ABT17041 (1-1547)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGTTGGCGCGGACCCGCTGCTTCTAGCGTTGCTGCTTCCCGAGTCTCTCTGGCGCGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAsnSerSerGlyArg 40
Db 384 GCGGCTGGCTCTGTTCCGAGCTGGCGCGCAGGAAGTTTCGGCGCGCGCTCGTTCGGCGCGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCTCCAGCCCTCTGACGAGTCTGACGAGTTTCGAGTTTCGGCTGCTTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 504 TTCGCCCTGAACAACAGAGACCCACCCCGAGCGGAGCGGTGCTGCCCTTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGCAGCACTCAGGTCAAGTCAGCGCGGCTCACCGCGCCACAGACACCGGTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGlu 120
Db 624 AGGCAGCCAGCCGAGGCAACACTGTGCGAGCTTCCACCATGAAGAATCTTTTGAAGAA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCGAAACGAGTGGGAAACAACCCGAGATCTTCTTTAATTAATTTATATCTATCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGAGTGTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAAACAGATGCAAGATGT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisGluIleAsnIleTyrGluIleIleLysProAla 180
Db 804 TTAGGAAACAATAGCAGTTCATCACCGAATTAATATTTATGAATCATAAACCTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACTCGAAATTCCTCCGTGACCAAGCTTTTGGACACAGGTTGGTGATCAGAT 923
Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
Db 924 GCAAGCAGTGGGAAAGTTTTGATGTCAACCCCGCTGTGATGCGGTGGAGTCGACAGGGA 983
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCACTGGATTCTGTTGGTGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGACACATGTAGATGATGACAGGTCTTTTGACCAAGATGAACACAGCTGGTGCACAGA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTGCTAGTAACCTTTTGGCCATGATGTAAGGAGGATCTCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAACGTCAGGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAGAGACACCT 1223


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Qy 301 LeuTyrVallePheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTTCAGTACGCTGGGGTGGGAATGACTGGATTGTGGCTCCCGGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCCCTTTACTGCCACGGAGATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerIleProLyAlaCys 360
Db 1344 AATCATGCCATTGTTCAGACGCTTGGTCAACTCTCTTAACCTTAAGATTCTTAAGGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluIleVal 380
Db 1404 TGTGTCCCGACAGAACTACAGTCTATCTCGATGCTGTACCTTTGACGAGAAATGAAGGTT 1463
Qy 381 ValLeuIleYsAntYrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTGTGGGTCTGCG 1511

RESULT 13
ID ADL13510 standard; DNA; 1547 BP.
XX AC ADL13510;
XX DT 06-MAY-2004 (first entry)
XX DE Osteoarthritis-associated polymorphic nucleotide #42.
XX KW ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
XX KW joint space narrowing; osteophyte development; joint pain;
XX KW osteoarthritis; SNP; single nucleotide polymorphism.
XX OS Homo sapiens.
XX PN WO2003054166-A2.
XX PD 03-JUL-2003.
XX PF 19-DEC-2002; 2002WO-US041225.
XX PR 20-DEC-2001; 2001US-0342603P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Jones KA, Schafer A;
XX PS WPI; 2003-559141/52.
XX PT Determining susceptibility of an individual to joint space narrowing,
XX PT osteophyte development and/or joint pain comprises identifying whether
XX PT the individual has at least one polymorphism in a polynucleotide encoding
XX PT a protein.
XX PS Disclosure; SEQ ID NO 42; 297pp; English.
XX CC The invention relates to a method of determining susceptibility of an
XX CC individual to joint space narrowing and/or osteophyte development and/or
XX CC joint pain comprising identifying whether the individual has at least one
XX CC polymorphism in a polynucleotide encoding at least one of the protein
XX CC listed in the specification. The methods, composition and agent are
XX CC useful for modulating the susceptibility of an individual to joint space
XX CC narrowing and/or osteophyte development and/or joint pain that is
XX CC associated with a disease, preferably osteoarthritis. The cell line and
XX CC the non-human animal are useful for screening for an agent for diagnosing
XX CC an individual having susceptibility to joint space narrowing and/or
XX CC osteophyte development and/or joint pain. This sequence corresponds to
XX CC the polynucleotide encoding a protein listed in the specification. (Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences).
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SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,2e-174 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-801-648-2 (1-396) x ADL13510 (1-1547)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
Db 324 ATGGTGGCCGGGACCCCGCTGTCTTCTAGCGTTGTCTCCCGAGGTCTCTCTGGGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgGlyPheAlaAlaAlaSerSerGlyArg 40
Db 384 GCGGCTGGCTCGTTCGGAGCTGGGCGGAGGAGTTCCGGGGGGTCTCGGGCGGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCCTCATCCAGGCCCTCTGACGAGTCTCTGAGCGAGTTCGAGTTGCGGTGCTCAGCATG 503
Qy 61 PheGlyLeuIleYsGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 504 TTCGGCTCGAAACAGAGACCCACCCCGAGGAGCGCGTGTGGTGGCCCTCATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACTGTATCGCAGGCACTCAGTCCAGCGGGTCCACCCGCCCGACACCCGGTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
Db 624 AGGCGAGCCAGCGAGCAACACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAAAGAA 683
Qy 121 LeuProGluThrSerGlyIleThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCGAAGAACGAGTGGGAAACAAACCCGAGATCTCTTTAATTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGACACAGATGCAAGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 804 TTAGGAAACAAATAGCAGTTCATCCATCACCGAATTAATATATTAATAATCATATAAACCTGCA 863
Qy 181 ThrAlaAsnSerIleYsPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACTCGAAATTCCTCCGTGACCGAGACTTTTGACACACAGGTGGTGAATCAGAT 923
Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 924 GCAGCAGGTGGGAAAGTTTGTATGTCACCCCGCTGTGATCGGTGAGTGCACACGGA 983
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluIleValSer 240
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Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGAGACATGTGTAGGTAAGCAGGTCTTTGCCAAGATGAACACAGCTGCTGCACAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGCCCATGTGTAGTAACCTTTTGGCCATGATGGAAAGGCACTCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuIleYsSerSerCysLysArgHisPro 300
Db 1164 AAACGTCAAGCCAAACAAACAGCGGAAACCGCTTAAGTCCAGCTGTGAAGAGACACCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
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Db 1224 TTGACGTGGACTTCAGTGACGCTGGGTGGATGACTGGATGTGTGCTCCCGGGGTAT 1283
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Db 1284 CACGCGCTTTTACTGCGCAGGAGAAAGCCCTTTTCTCTGGCTGATCATCTGAACCTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 ATCATGCCATTTGTCAGACGTTGGTCAACTCTGTTAACTTCAAGTTCCTTAGGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCGACAGAACTCAGTCTATCTCGATGCTGTACCTTGACGAGATGAAAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGACATGCTTGTGGAGGTTGTGGGTGTGCG 1511
RESULT 14
ADN38841
ID ADN38841 standard; cDNA; 1547 BP.
XX
AC ADN38841;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:159.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-039775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Ariz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KB, Zlotnik A;
XX
XX WPI; 2003-468649/44.
DR P-PSDB; ADN38842.
XX
PT Determining the presence or absence of a pathological cell in a patient,

PT useful for diagnosing, prognosing or treating cancer, comprises detecting
XX a nucleic acid in a biological sample.
PS Claim 8; SEQ ID NO 159; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides, and
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.2e-174 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-801-648-2 (1-396) x ADN38841 (1-1547)
Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGTTGGCGCGGACCCGCTGCTTCTAGGTTGCTTCCCGAGGCTCTCTCGGCGCGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAspSerGlyArg 40
Db 384 GCGGCTGGCTCTGTTCCGAGCTGGGCGCGAGAAAGTTGCGGCGCGCGCTGTCGCGCGCGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCCAGCCCTCTGACGAGTCTTGACGAGTTCTGAGTTGCGGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 504 TTGGGCTGMAACACAGACAGACCCACCCAGCAGGAGCGGCTGTCGCCCTTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGCAGGCACTCAGGTCAGCGGGCTCACCAGCGCCAGACACCGGTTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGlu 120
Db 624 AGGGCAGCCAGCCGAGCCACCACTGTGGCAGCTTCCACCATGAGAAATCTTTGGAGAA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePhePheAsnLeuSerSerIlePro 140
Db 684 CTACCGAAGAACGAGTGGGAAACACACCCGAGATCTCTTCTTAATTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleLysProAla 180
Db 804 TTAGGAAACAATAGCAGTTTCATCACCGAATTAATATTATTAATATCAAAACCTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200

Db 864 ACAGCCAACTCGAAATTCCTCCCGTGACCAGACTTTTGGACACAGGTTGGTGAATCAGAAT 923
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Qy 221 HisAlaAenHisGlyPheValValGluValAlaHisIsteuGluGluLysGlnGlyValSer 240
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Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGAGACATGTAGGATAAGCAGGTCTTTTGACCAAGATGAACACAGCTGTGTACAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTGCTAGTAACATTTTGGCCATGATGGAAAGGGCATCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisGlnArgLysArgLysSerSerCysLysArgHisPro 300
Db 1164 AAGCTCAGGCACCAACACAAACAGCGGAAACGCTTTAAGTCCAGCTGTAAAGACACCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTGACGTGGGGTGGAAATGACTGATTTGGCTCCCGGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCCCTTTACTGTCACGAGAAATGCCCTTTCTCTGGTGTATCATCTGAACCTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 AATCATGCCATGTTCAGACGTTGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGGTTGTGGGTGTGCG 1511

RESULT 15

ADH11558
ID ADH11558 standard; cDNA; 1547 BP.
XX AC ADH11558;
XX DT 11-MAR-2004 (first entry)
XX DE Human bone morphogenic protein (BMP) polynucleotide #7.
XX KW Human; bone morphogenic protein; BMP; gene; ss; weight gain;
KW appetite suppression; fat mass reduction; cell sensitivity;
KW glucose uptake; diabetes; insulin resistance; hyperglycaemia;
KW hypertension; coronary artery disease; renal failure; neuropathy;
KW metabolic disorder; glucose metabolism disorder; endocrine disorder;
KW obesity; weight loss; liver disorder; cartilage growth disorder;
KW bone growth disorder; inflammation; aberrant cell growth; liver cancer.
XX OS Homo sapiens.
XX US2003224501-A1.
XX PD 04-DEC-2003.
XX PF 14-FEB-2003; 2003US-00366345.
XX FR 17-MAR-2000; 2000US-0190067P.
FR 16-MAR-2001; 2001US-00809269.
PR 23-MAR-2001; 2001WO-US009229.
PR 17-JAN-2002; 2002US-0348621P.
PR 22-JAN-2002; 2002US-0349356P.

PR 28-JAN-2002; 2002US-0351520P.
PR 06-FEB-2002; 2002US-0354265P.
PR 15-FEB-2002; 2002US-0356749P.
PR 16-JAN-2003; 2003US-00345236.
XX (YOUNG/) YOUNG P E.
XX (RUBE/) RUBEN S M.
XX Young PE, Ruben SM;
XX WPI; 2004-022075/02.
XX P-PSDB; ADH11579.
XX New bone morphogenic protein polypeptides and polynucleotides, useful for
diagnosing, preventing, treating or ameliorating a medical condition, e.g.
diabetes, dyslipidemia, hypertension, coronary artery disease or
neuropathy.
XX Example 1; SEQ ID NO 10; 224pp; English.
XX The invention relates to human bone morphogenic protein (BMP)
polypeptides and the polynucleotides encoding them. The invention also
relates to a method for limiting weight gain, suppressing appetite or
reducing fat mass, comprising administering to a mammalian subject a
therapeutic amount of a BMP polypeptide, and a method for increasing the
sensitivity of a cell to insulin or increasing glucose uptake by a cell,
comprising contacting the cell with a BMP polypeptide. The BMP
polypeptides and polynucleotides are useful for diagnosing a pathological
condition or a susceptibility to a pathological condition in a subject or
for preventing, treating or ameliorating a medical condition, e.g.
diabetes, insulin resistance, hyperglycaemia, hypertension, coronary
artery disease, renal failure, neuropathy, metabolic disorders, glucose
metabolism disorder, endocrine disorders, obesity, weight loss, liver
disorders, cartilage and bone growth disorders, inflammation or aberrant
cell growth such as liver cancer. The BMP polypeptides and
polynucleotides are also useful for regulating nutritional partitioning,
limiting weight gain, suppressing appetite, reducing fat mass, increasing
the sensitivity of a cell to insulin or increasing glucose uptake by a
cell. This sequence represents a human BMP polynucleotide of the
invention.
SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 U; 0 Other;

Alignment Scores:
Pred. NO.: 6.2e-174 Length: 1547
Score: 2099.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-801-648-2 (1-396) x ADH11558 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
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Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
Db 384 GCGGCTGGCTCGTTCTCGAGCTGGCGCGCAGGAAGTTTCGCGCGCGCTGCTCGGCGCGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCCAGGCCCTCTGACAGGTCCTGAGCGAGTTTCAGATTGCGGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetIeu 80
Db 504 TTGGGCTTGAACAGAGACCCACCCCGACGAGGAGCGCGTGTGTCCTCCCTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGAGGCACTCAGGTTCAGGTCAGCGGGCTCACCCTCGCCCGCCAGACCA 623

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Qy	121	Leu	Pro	Glu	Thr	Ser	Gly	Leu	Thr	Arg	Arg	Phe	Phe	Asn	Leu	Ser	140
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Db	924	GCA	AG	CAG	TGTGG	AA	AGTTT	TG	ATGT	CA	CCCC	CGCTGT	GTAT	GCGGTG	GA	CTG	983
Qy	221	His	Ala	Asn	His	Gly	Phe	Val	Val	Glu	Val	Ala	His	Leu	Glu	Glu	240
Db	984	CAC	SC	CA	ACC	ATG	AT	TG	TG	TG	GA	AGTGG	CCCC	CAC	TTG	GAG	1043
Qy	241	Lys	Arg	His	Val	Arg	Leu	Ser	Arg	Ser	Leu	His	Gln	Asp	Glu	His	260
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Qy	261	Arg	Pro	Leu	Leu	Val	Thr	Phe	Gly	His	Asn	Gly	Ser	Gly	His	Pro	280
Db	1104	AGG	CA	TG	CTAG	TAA	CTTT	TGG	CCAT	GTAT	G	TA	GA	AAAG	GG	CA	1163
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Qy	321	His	Ala	Phe	Tyr	Cys	His	Gly	Gly	Cys	Pro	Phe	Pro	Leu	Ala	Asp	340
Db	1284	CAC	GC	CTTT	TAC	TG	CC	CA	CGG	AA	TG	CC	CTTT	TCT	TG	CT	1343
Qy	341	Asn	His	Ala	Leu	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Leu	360
Db	1344	AAT	CA	TG	CC	AT	TG	T	CA	G	CTT	G	T	TA	CT	T	1403
Qy	361	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Leu	Ser	Met	Leu	Tyr	Leu	Asp	380
Db	1404	TGT	GT	CC	CG	CA	GA	AA	CT	CAG	TG	CT	AT	CT	CG	AT	1463
Qy	381	Val	Leu	Lys	Asn	Tyr	Gln	Asp	Met	Val	Glu	Gly	Cys	Gly	Cys	Arg	396
Db	1464	GT	AT	TAA	GA	ACT	AT	CAG	CA	TG	TTG	TG	GAG	GGT	TG	GG	1511

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2006, 23:43:25 ; Search time 177 Seconds
(without alignments)
3976.918 Million cell updates/sec

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Perfect score: 2098
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 2000000000
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Issued Patents NA:

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- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
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- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2098	100.0	1547	2	US-08-377-292-2
2	2098	100.0	1607	3	US-07-721-847A-3
3	2098	100.0	1607	3	US-08-925-779-3
4	2098	100.0	1607	3	5166058-3
5	2098	100.0	3526	3	US-09-976-594-11
6	2095	99.9	1607	3	US-07-989-847-1
7	2095	99.9	1607	3	US-08-469-411-1
8	2095	99.9	1607	3	US-09-780-601A-1
9	2092	99.7	1260	2	US-07-841-646-4

10	2092	99.7	1260	2	US-07-901-703-14	Sequence 14, Appl
11	2092	99.7	1260	2	US-08-147-023-4	Sequence 4, Appl
12	2092	99.7	1260	2	US-08-447-570-4	Sequence 4, Appl
13	2092	99.7	1260	2	US-08-449-700-4	Sequence 4, Appl
14	2092	99.7	1260	2	US-08-449-699A-4	Sequence 4, Appl
15	2092	99.7	1260	3	US-09-148-925C-4	Sequence 4, Appl
16	2092	99.7	1260	3	US-08-957-425-4	Sequence 4, Appl
17	2092	99.7	1260	3	US-10-321-799-4	Sequence 4, Appl
18	2092	99.7	1260	6	PCT-US93-05446-14	Sequence 14, Appl
19	2092	99.7	1607	2	US-07-679-451-1	Sequence 1, Appl
20	2092	99.7	2185	3	US-09-949-016-4668	Sequence 4668, Ap
21	2043.5	97.4	1314	3	US-08-713-556P-39	Sequence 39, Appl
22	1796.5	85.6	1233	2	US-08-362-670B-27	Sequence 27, Appl
23	1796.5	85.6	1233	3	US-08-333-376C-27	Sequence 27, Appl
24	1796.5	85.6	1233	3	US-08-808-324-27	Sequence 27, Appl
25	1796.5	85.6	1233	3	US-09-945-182-27	Sequence 27, Appl
26	1796.5	85.6	1233	6	PCT-US94-14030A-27	Sequence 27, Appl
27	1542	73.5	1992	2	US-08-455-550-6	Sequence 6, Appl
28	1511	72.0	14759	3	US-09-661-887-1	Sequence 1, Appl
29	1505	71.7	15203	3	US-09-949-016-16410	Sequence 16410, A
30	1412.5	67.3	15144	3	US-08-458-434A-6	Sequence 6, Appl
31	1269	60.5	1751	2	US-08-377-292-4	Sequence 4, Appl
32	1269	60.5	1788	2	US-07-841-646-6	Sequence 6, Appl
33	1269	60.5	1788	2	US-07-901-703-18	Sequence 18, Appl
34	1269	60.5	1788	2	US-08-147-023-6	Sequence 6, Appl
35	1269	60.5	1788	2	US-08-447-570-6	Sequence 6, Appl
36	1269	60.5	1788	2	US-08-449-700-6	Sequence 6, Appl
37	1269	60.5	1788	2	US-08-449-699A-6	Sequence 6, Appl
38	1269	60.5	1788	3	US-09-148-925C-6	Sequence 6, Appl
39	1269	60.5	1788	3	US-08-957-425-6	Sequence 6, Appl
40	1269	60.5	1788	3	US-10-321-799-6	Sequence 6, Appl
41	1269	60.5	1788	6	PCT-US93-05446-18	Sequence 18, Appl
42	1269	60.5	1945	3	US-09-949-016-1476	Sequence 1476, Ap
43	1269	60.5	1954	2	US-08-050-132A-3	Sequence 3, Appl
44	1269	60.5	1954	2	US-07-989-847-3	Sequence 3, Appl
45	1269	60.5	1954	3	US-08-750-222A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-08-377-292-2
; Sequence 2, Application US/08377292
; Patent No. 5693615
; GENERAL INFORMATION:
; APPLICANT: STONE, ROGER L.
; TITLE OF INVENTION: THERAPEUTIC FORMULAS FOR OSTEOINDUCTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Procter & Gamble Company
; STREET: 11810 East Miami River Road
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 45239-8707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,292
; FILING DATE: 23-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/08/243,435
; FILING DATE:
; APPLICATION NUMBER: US/08/117,367
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Corstanje, Brahm J.
; REGISTRATION NUMBER: 34,804
; TELECOMMUNICATION INFORMATION:


```
;
; TELEPHONE: 513-245-2858
; TELEFAX: 513-741-3012
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1547 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-377-292-2

Alignment Scores:
Pred. No.: 3,44e-200 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-801-648-2 (1-396) x US-08-377-292-2 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGTTGGCGCGGACCCGCTGCTTCTAGCGTTGCTTCCCAAGGTCCTCTGGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaSerSerGlyArg 40
Db 384 CGGCTGGCGCTGCTTCCGAGCTGGCGCGCAGGAGTTCCGCGCGCGCTGCTGGGCGGC 443
Qy 41 ProSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCCAGCCCTCTGACGAGTCTGACGAGTTCCGAGTTGCGGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgPheAlaValValProProTyrMetLeu 80
Db 504 TTCGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGTGCTCCCTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCCAGGACCTCAGGTGACCGCGGCTACCCCGCCCGCAGACCCGCGTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGCGAGCAGCCGAGCCAACTGTGCGCAGCTTCCACCATGAAGATCTTTGGAAGA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCAAGAACGAGTGGGAAACCAACCGGAGATTTCTTTAAATTTAAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGAGGTTTATCACTCTCAGCAGAGCTTCAGGTTCGAGAACACAGATGCAAGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 804 TTAGAAACATAGAGTTTCCATCCAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACCTCGAAATCCCGCGTACCAAGATTTTGGACACACAGGTTGGTGAATCAGAA 923
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 924 GCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGATGCGGTGGACTGCAAGGGA 983
Qy 221 HisAlaAsnHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCATGGATTCGTGGTGAAGTGGCCCACTTGGAGGAGAAACAGGTTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGAGACATGTTAGGATTAAGCAGGTCTTTTGCCCAAGATGAACAGCTGCTGCACAGATA 1103
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Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAAGGGCATCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAACGTCAGGCCAAACACAAACAGCGGAAACGCTTAAGTCCAGCTCTGAAGAGACACCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTrpIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTTCAGTGGCGGTGGAACTGGATTTGGTCTCCCGGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CAGCCCTTTTACTGCCACGAGGAAATGCCCTTTTCTCTGGCTGATCATCTGAACTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerIleProLysAlaCys 360
Db 1344 AATCATGCCATTGTTCAAGCGTTGGTCAACTCTGTTAACTCTAAGATTCCTAAGGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrIleuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAAATGAAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTTGGAGGGTTTGGGTGCTGC 1511

RESULT 2
US-07-721-847A-3
; Sequence 3, Application US/07721847A
; Patent No. 6150328
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: No. 6150328el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/721,847A
; FILING DATE: 14-JUN-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: 5160C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; CELL TYPE: Osteosarcoma Cell Line
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; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; CELL TYPE: Osteosarcoma Cell Line
; CELL LINE: U-2OS
; IMMEDIATE SOURCE:
; LIBRARY: U2OS cDNA in Lambda GT10
; CLONE: Lambda U2OS-39
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1546
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1202..1543
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 14..1607
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 356..424

US-08-925-779-3

Alignment Scores:

Pred. No.: 3.64e-200 Length: 1607
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-801-648-2 (1-396) x US-08-925-779-3 (1-1607)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuGlyGly 20
Db 356 ATGTGTCGCGGAGCCCGCTGCTTCTAGCGTGTCTTCCCGAGGTCCTCTCGGCGGC 415
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaSerSerGlyArg 40
Db 416 GCGGCTGGCCTCGTTCGGAGCTGGCGCGCAGGAAGTTTCGCGCGCGCTCTCGGCGGC 475
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 476 CCCTCATCCAGCCCTCTGACGAGCTCTGACGAGTTCGAGGTTCCGAGTCTCAGCATG 535
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 536 TTCGGCTGAAACAGAGACCCACCCCGCAGGACGCGCGTGGTCCCGCCCTACATGCTA 595
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCGAGGCACTCAGGTCAGCGGGCTCACCCGCGCCAGACCACCGGTTGGAG 655
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 656 AGGCGAGCAGCCGACCACTGTGCGCAGCTTCACCATGAAGAATCTTTGGAAGAA 715
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 716 CTACAGAAACGAGTGGGAAACAAACCCGAGATTCCTTTTAATTTAAGTTCATCCCC 775
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 776 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 835

Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 836 TTAGGAACAATAGCAGTTTCCATCACCGAATTAATATTTATGAATCATATAACCTGCA 895
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 896 ACAGCCAACCTCGAAATTCCTCGTACCAGACTTTTGACACACAGGTTGGTGAATCAGAT 955
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 956 GCAGCAGGTGGGAAAGTTTGTATGTCACTCCCGCTGTGATCGCGTGAGCTGCACAGGA 1015
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1016 CACGCCAACCATGATTCGTGTGAAAGTGGCCCACTTGGAGGAGAAACAGGTGTCTCC 1075
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTTPSerGlnIle 260
Db 1076 AAGAGACATGTTAGGATAAGCAGGTCTTTGGCCATGATGGAAGAGGCATCTCTCCACAAAGAGAA 1135
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1136 AGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGAGGCATCTCTCCACAAAGAGAA 1195
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1196 AACGTCAAGCCAAACACAAACAGCGGAAAGCGCTTAAGTCCAGCTGTAAAGAGACACCT 1255
Qy 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTTPileValAlaProProGlyTyr 320
Db 1256 TTGTACGTGGACTTCAGTGACGTGGGTGGAATGACTGGATTTGGCTTCCCTCCCGGGGTAT 1315
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1316 CACGCTTTTACTGCCACGAGAAATGCCCTTCTCTGGCTGATCATCTGAACCTCCACT 1375
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1376 AATCATGCCATTGTTCAAGCGTTGTCACACTCTCTTAACCTCTAAGATTCTTAAGGCATGC 1435
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1436 TGTGTCGCGACAGAACTCAGTGCTATCTCGATGCTGACCTTGACGAGAAATGAAGAAGTT 1495
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAGAAGCAATATCAGGACATGTTGTGGAGGTTGTGGGTCTGCG 1543

RESULT 4

5166058-3
; Patent No. 5166058
; APPLICANT: WANG, ELIZABETH A.; WOZNEY, JOHN M.; RPSEN, VICKI A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING THE OSTEOINDUCTIVE
; PROTEINS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/378,537
; FILING DATE: 11-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 179,100
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: 28,285
; FILING DATE: 20-MAR-1987
; APPLICATION NUMBER: 943,332
; FILING DATE: 17-DEC-1986
; APPLICATION NUMBER: 880,776
; FILING DATE: 01-JUL-1986
; SEQ ID NO: 3:
; LENGTH: 1607
5166058-3

Alignment Scores:

Pred. No.: 3,648-200 Length: 1607
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-801-648-2 (1-396) x 5166058-3 (1-1607)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
DB 356 ARGGGCGGCGGACCGCTCTTCTAGCGTTGCTTCCCGAGGCTCTCTCGGCGGC 415

QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgGlyPheAlaAlaSerSerGlyArg 40
DB 416 GCGGCTGCTGTTCCGGAGTGGCGCCAGAGAGTTCCGCGCGGCTGCTCGGCGGC 475

QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
DB 476 CCTCATCCAGCCCTCTGACGAGGCTCTGACGAGTTCGAGTTCGAGTTCGAGCATG 535

QY 61 PheGlyLeuLeuGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
DB 536 TTCGGCTGAAACAGAGACCCACCCAGCAGGACCGCGTGTGCTCCCTACATGCTA 595

QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
DB 596 GACCTGTATCGAGGACCTCAGTTCAGCGGGCTCACCGCCCGAGACCCCGTTGAG 655

QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGlu 120
DB 656 AGGCGAGCCAGCGGACCAACTGTGCGAGCTTCCACCATGAAGATCTTTGGAAGA 715

QY 121 LeuProGluThrSerGlyLeuThrArgArgPhePheAsnLeuSerSerIlePro 140
DB 716 CTACAGAAACAGAGTGGGAAACAAACCCGAGATCTCTCTTTAAATTAAGTTCTATCC 775

QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
DB 776 ACGGAGGAGTTTATCACCTCAGCAGGCTTCAAGTTTCCGAGAACAGATGCAATGCT 835

QY 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLeuProAla 180
DB 836 TTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATATTAATGAAATCAATAAACCTGCA 895

QY 181 ThrAlaAsnSerIlePheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
DB 896 ACAGCCAACTCGAAATTCCTCCGTGACCCAGACTTTTGGACACCCAGGTTGCTGAATCAGAAT 955

QY 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGly 220
DB 956 GAAGCAGGTGGGAAGTTTTCATGTACACCCCGCTGTGATCGCGTGAAGTGCACAGGA 1015

QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLeuGlyValSer 240
DB 1016 CACGCCAACCATGGATTCTGTGTGGAGTGGCCACTTGGAGAGAAACAGGTGTCTCC 1075

QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
DB 1076 AAGAGACATGTTAGGATAGCAGGTCTTTGACCAAGATGAACACAGCTGTGTACAGATA 1135

QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
DB 1136 AGGCCATGCTAGTAATCTTTTGCCCATGTATGAAAGGGGCATCTCTCCACAAAAGAGAA 1195

QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
DB 1196 AAACGTCAAGCCAAACACAAACAGCGGAAACCGCTTAACTCCAGCTGTAAAGAGACACCT 1255

QY 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
DB 1256 TTGTAGCTGACTTCACTGACGTGGGTGGAATGACTGATGTTGGCTCTCCCGGGGTAT 1315

QY 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
DB 1316 CACGCTTTTACTGCGACGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAATCTCCACT 1375

QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerIlePheProLysAlaCys 360
DB 1376 AATCATGCCATGTTTCAGACGTTGCTCAACTCTGTAACTCTAAAGATTCCTTAAGCATGC 1435

QY 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
DB 1436 TGTGTCCCGACAGAACTCAGTCTATCTGATCTGTACCTTGACGAGAAATGAAAGGTT 1495

QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
DB 1496 GTATTAAAGAACTATCAGACATGTTGTGGAGGTTGTGGGTGTGCG 1543

RESULT 5

US-09-976-594-11
; Sequence 11, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 3526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1016903.1

US-09-976-594-11

Alignment Scores:
Pred. No.: 1,198-199 Length: 3526
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-801-648-2 (1-396) x US-09-976-594-11 (1-3526)

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DB 1180 ATGGTGGCGGCGGACCGCTGCTTCTAGCGTTGCTTCCCGAGGCTCTCTCGGCGGC 1239

QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgGlyPheAlaAlaSerSerGlyArg 40
DB 1240 GCGGCTGCTGCTTCCCGAGCTGGCGCGCAGAGAGTTCCGCGCGGCTGCTCGGCGGC 1299

QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
DB 1300 CCTCATCCAGCCCTCTGACGAGGCTCTGACGAGTTCGAGTTCGAGTTCGAGCATG 1359

QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
DB 1360 TTCGGCTGAAACAGAGACCCACCCAGCAGGACCGCGTGTGCTCCCTACATGCTA 1419

QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
DB 1420 GACCTGTATCGAGGACCTCAGTTCAGCGGGCTCACCGCCCGAGACCCCGTTGAG 1479

QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGlu 120
DB 1480 AGGCGAGCCAGCGGACCAACTGTGCGAGCTTCCACCATGAAGATCTTTGGAAGA 1539

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Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAenLeuSerSerIlePro 140
Db 1540 CTACAGAAACGAGTGGGAAACAAACCGGAGATTCCTCTTTAATTTAAAGTTCTATCCCC 1599
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 1600 ACGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 1659
Qy 161 LeuGlyAenAenSerSerPheHisArgIleAenIleThrGluIleLeuLysProAla 180
Db 1660 TTAGGAAACATAGCAGTTCCATCACCAGATTAATATTTATGAATCATATAAACCTGCA 1719
Qy 181 ThrAlaAenSerLysPheProValThrArgLeuLeuAspThrArgLeuValAenGlnAen 200
Db 1720 ACAGCCAACTCGAAATTCCTCGTACCCAGACAGCTTTTGACACACAGGTTGGTGAATCA 1779
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Db 1780 GCAAGCAGTGGGAAAGTTTGTATGTACCCCGCTGTGATCGGTGGACTGCACAGGA 1839
Qy 221 HisAlaAenHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1840 CACGCCAACCATGATTCGTGTGAGAGTGCCCACTTGGAGGAGAAACAAAGGTGTCTCC 1899
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1900 AAGAGACATGTAGGATTAAGCAGGTCTTTTGACCAAGATGAACACAGCTGGTCTACAGTA 1959
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1960 AGGCATTTGTAGTAATCTTTTGGCATGATGGAAGGGCATCTCTCCACAAAGAGAA 2019
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 2020 AAACGTCAAGCCAAACACAAACAGCGGAAACGCCTTAAGTCCAGCTGTGAAGACACCCCT 2079
Qy 301 LeuThrValAspPheSerAspValGlyTrpAenAspTrpIleValAlaProProGlyTyr 320
Db 2080 TTGTACGTGGACTTTCAGTGACGTGGGTGGGAATGACTGGATTTGGTCTCCCGGGGTAT 2139
Qy 321 HisAlaPheTyrCysHisGlyCysProPheProLeuAlaAspHisLeuAenSerThr 340
Db 2140 CACGCTTTTACTGCCACGAGAAATGCCCTTTTCTCTGGCTGATCATCTGAATCTCACT 2199
Qy 341 AenHisAlaIleValGlnThrLeuValAenSerValAenSerLysIleProLysAlaCys 360
Db 2200 AATCATGCCATTGTTCAGACGTTGGTCAACTCTGTAACTCTAAGATTCTCTAAGGCATGC 2259
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAenGluLysVal 380
Db 2260 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGAAATGAAGAAGTT 2319
Qy 381 ValLeuLysAenTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 2320 GTATTAAAGAACTATCAGACATGTTGTGAGGGTGTGGGTGTGCG 2367
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RESULT 6

US-07-989-847-1

; Sequence 1, Application US/07989847

; Patent No. 5863364

; GENERAL INFORMATION:

; APPLICANT: Israel, David

; APPLICANT: Wolfman, Neil M.

; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein

; TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

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; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07989,847
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI-5192B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1543
; US-07-989-847-1
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Alignment Scores:

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Pred. No.: 7,27e-200 Length: 1607
Score: 2095.00 Matches: 395
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.86% Indels: 0
DB: 2 Gaps: 0
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US-10-801-648-2 (1-396) x US-07-989-847-1 (1-1607)

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Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAspSerGlyArg 40
Db 416 GCGGCTGGCTCGTTCGCGAGCTGGGCGCAGGAAGTTGCGGCGCGCTCTCGGCGCGC 475
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 476 CCCTCATCCAGCCCTCTGACGAGTCTTGACGAGTTGAGTTGCGGCTGCTCAGCATG 535
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 536 TTCGGCTGAAAACAGAGACCCACCCCGCAGGAGCGCGTGTGTGCGCCCTACATGCTA 595
Qy 81 AspleuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCGCAGGCACCTCAGGTCAGCCCGGCTCACC CGGCCCCAGACCACCGGTGAG 655
Qy 101 ArgAlaAlaSerArgAlaAenThrValArgSerPheHisGluGluSerLeuGluGlu 120
Db 656 AGGCACGCCAGCCGAGCAACACTGTGCGGAGCTTCCACCATGAGAAATCTTTGGAAGAA 715
Qy 121 LeuProGluThrSerGlyLysThrArgArgPhePheAenLeuSerSerIlePro 140
Db 716 CTACCAGAAACGAGTGGGAAAAACAACCGGAGATTCCTCTTAATTTAAAGTTCTATCCCC 775
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 776 ACGGAGGAGTTTATCACCCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATCAAGATGCT 835
Qy 161 LeuGlyAenAenSerSerPheHisArgIleAenIleThrGluIleLeuLysProAla 180
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836 TTAGGAAACAATAGCAGTTTCATCCACCGAAATTAATATTTATGAATCATATAAACCTGCA 895
181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
896 ACAGCAACTCGAAATCCCGTGACACAGACTTTTGGACACAGAGTTGGTGAATCAGAAT 955
201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
956 GCAAGCAGTGGAAACTTTTGATGTACCCCGCTGTGATGGGTGACGTGCACAGGA 1015
221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
1016 CACGCCAACCACTGATTCGTGTGAAGTGGCCACTTTGGAGGAGAAACAAGGTGTCTCC 1075
241 LysArgHisValArgLysSerArgSerLeuHisGlnAspGluHisSerTTPSerGlnIle 260
1076 AAGACACATGTAGATAGCAGGTCTTGGACCAAGATGAACACAGCTGGTGCACAGATA 1135
261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
1136 AGGCCATTGCTAGTAACCTTTGGCCATGATGGAAAGGCATCTCTCCACAAAGAGAA 1195
281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
1196 AAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAGAGACACCT 1255
301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTTPAlaValAlaProGlyTyr 320
1256 TTGTACGTGGACTTCAGTGACGTGGGTGGATGATGTGGCTTGGCTCCCGGGGTAT 1315
321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
1316 CACGCTTTTACTGCGACGGAATGCGCTTTCTCTGGCTGATCATCTGACTCCACT 1375
341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
1376 AATCATGCCATTGTTTACAGCTGCTCAACTCTGTTAACTCTTAAGATTCTTAAGGCATGC 1435
361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
1436 TGTGTCCGACAGAACTCAGTCTATCTCGATGCTGTACCTTGCAGCAGAAATGAAGAAGTT 1495
381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysArgCysArg 396
1496 GTATTAAAGACTATCAGACATGTTTGTGGAGGTTTGTGGGTGCGC 1543

RESULT 7

US-08-469-411-1
; Sequence 1, Application US/08469411
; Patent No. 6190880
; GENERAL INFORMATION:
; APPLICANT: Israel, David
; Wolfman, Neil M.
; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
; Heterodimers, Compositions and Methods of Use.
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,411
; FILING DATE: 06-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:

NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/POCKET NUMBER: GI-5192B-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8622
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 356..1543
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-469-411-1
Alignment Scores:
Pred. No.: 7,27e-200 Length: 1607
Score: 2095.00 Matches: 395
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.86% Indels: 0
DB: 3 Gaps: 0

US-10-801-648-2 (1-396) x US-08-469-411-1 (1-1607)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly 20
Db 356 ATGTGGCGGGACCGCTGCTTCTAGCGTTGCTGCTCCAGGTCTCTCTGGCGGC 415
QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
Db 416 CGCGTGCCTCGTTCCGAGCTGGCGCGCAGAGATTCCGCGCGCGCTGCTGGCGCGC 475
QY 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 476 CCTCATCCAGCCCTCTGACGAGTCTCTGACGAGTTCCGAGTTGCGGCTGCTCAGCATG 535
QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 536 TTGCGCTGAAACAGAGACACCCAGAGAGGAGCGCGTGGTCCCGCTTACATGCTTA 595
QY 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCGCAGCACTCAGGTGAGCGGCTCAGCGCGCCAGACCCCGGTGGAG 655
QY 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 656 AGGCGACGCGCGGACCACTGTGCGAGCTTCCACCATGAAGATCTTTGGAGAA 715
QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 716 CTACCAGAAACGAGTGGGAAACACACCGGAGATTCTTTTAAATTTAAGTTCTATCCC 775
QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 776 ACGGAGGAGTTTATCACCTCAGCAGAGCTTTCAGGTTTCCGAGAAACAGATGCAATGCT 835
QY 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleLysProAla 180
Db 836 TTAGGAAACAATAGCAGTTTCCATCACCAGATTAATATTTATGAATCATATAAACCTGCA 895
QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 896 ACAGCAACTCGAAATCCCGTGACACAGACTTTTGGACACAGAGTTGGTGAATCAGAAT 955
QY 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 956 GCAAGCAGTGGAAACTTTTGTATGTCTACCCCGCTGTGATGCGGTGGAGTCTCAGAGGA 1015


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Qy 221 HisAlaAenHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
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Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
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Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1316 CACGCCTTTTACTGCGACGGAATGCCCTTTTCTCTGGCTGATCATCTGAACCTCCACT 1375
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Db 1436 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGATGAAGAAGTT 1495
Qy 391 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG 1543
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RESULT 8

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US-09-780-601A-1
; Sequence 1, Application US/09780601A
; Patent No. 6593109
; GENERAL INFORMATION:
; APPLICANT: Israel, David
; APPLICANT: Wolfman, Neil M.
; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
; TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/780,601A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,411
; FILING DATE: 06-Jun-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI-5192B-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8622
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1543
US-09-780-601A-1
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Alignment Scores:

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Pred. No.: 7.27e-200 Length: 1607
Score: 2095.00 Matches: 395
Percent Similarity: 100.00% Conservatve: 1
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.86% Indels: 0
DB: 3 Gaps: 0
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US-10-801-648-2 (1-396) x US-09-780-601A-1 (1-1607)

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Db 356 ATGCTGGCGCGACCCGCTGCTTCTAGCGTTGCTTCCAGGTCTCTCTGGCGGC 415
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLysSerSerGlyArg 40
Db 416 GCGGCTGGCTCGTTCGCGAGCTGGCGCGCAGGAGTTCCGCGCGCGTCTCTGGCGGC 475
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 476 CCCTCATCCAGCCCTCTGACAGGTCTTGACGAGTTGAGTTGCGGCTGCTCAGCATG 535
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 536 TTCGGCTGAAACAGAGACACCCACCCAGCAGGAGCGCGGTGTGCGCCCTACATGCTA 595
Qy 81 AspleuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 596 GACCTGTATCGCAGGCATCTCAGGTGACCGCGGCTCACCCGCCAGACACCCGTTGAG 655
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Db 656 AGGCAGCCAGCCGAGCCACACATGTGCGGAGCTTCCACCATGAAGAATCTTTGGAGAA 715
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 716 CTACCAGAAACGAGTGGGAAAAACAACCGGAGATTCTCTTTAATTTAAGTTCTATCCCC 775
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 776 ACGGAGGAGTTTATCACCTCAGCAGAGCTTTCAGGTTTTCCGAGAACACAGATCAAGATGCT 835
Qy 161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleLeuLysProAla 180
Db 836 TTAGAAACAAATAGCAGTTTCCATCAGCAATTAATTTATGAATCATTAACCTGCA 895
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 896 ACAGCCAACTCGAAATTTCCCGTGACACAGACTTTTGGACACACAGGTTGGTGAATCAGAAT 955
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Db 956 GCAAGCAGGTGGGAAACCTTTTGAATGTACCCCCCTGTGATGCGGTGAGCTGCAAGGGA 1015
Qy 221 HisAlaAsnHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 1016 CACGCCAACCATGATGATTCGTGGTGAAGTGCCCACTTGGAGGAAACAAGGTGTCTCC 1075
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1076 AAGAGACATGTTAGGATTAAGCAGGTCTTTGACCAAGATGAACACAGCTGCTCACAGATA 1135
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QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
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QY 281 LysArgGlnAlaLysHisGlnArgLysArgLysSerSerCysLysArgHisPro 300
Db 1196 AAACGTCAGGCCAAACACAAACAGCGGAACGCTTAAAGTCCAGCTGTAAGAGACACCCCT 1255
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Db 1436 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGATGAAGAGTT 1495
QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1496 GTATTAAAGAACTATCAGACATGTTGTGGAGGGTGTGGGTGTGCG 1543

RESULT 9

US-07-841-646-4
; Sequence 4, Application US/07841646
; Patent No. 5266683
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H. L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESS: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/841,646
; FILING DATE: 19920221
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374

FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: FITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: CDS
LOCATION: 9..1196 /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "CBMP2A"
OTHER INFORMATION: /note= "CBMP2A (CDNA)"
US-07-841-646-4

Alignment Scores:
Pred. No.: 1,01e-199 Length: 1260
Score: 2092.00 Matches: 395
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
DB: 2 Gaps: 0
US-10-801-648-2 (1-396) x US-07-841-646-4 (1-1260)

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QY 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaSerSerGlyArg 40
Db 69 GCGGCTGGCCCTCGTTCCGAGCTGCGCGCGCGAGAAAGTTTCGCGCGCGCGC 128
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Db 129 CCTCATCCAGCCCTCTGACGAGGTCTGACGAGTTCGAGTTGCGGCTGCTCAGCATG 188
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 189 TTCGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGTGCCCCCTACATGCTA 248
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 249 GACCTGTATCGACGCACTTCGGGTGAGCCGGGCTCACCCGCCCCAGACCCAGCGTGGAG 308
Qy 101 ArgAlaLaserArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
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Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAenLeuSerSerIlePro 140
Db 369 CTACCAAGACGAGTGGGAAACACACCGGAGATCTTCTTAATTTAAGTTCTATCCCC 428
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Db 429 ACAGGAGAGTTATACCTCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATCAAGATGCT 488
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Db 489 TTAGGAACATAGCAGTTTCCATCACCAGATTAATTAATTAAGATCAATAAACCTGCA 548
Qy 181 ThrAlaAenSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAen 200
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Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
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Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 789 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGGAGGATCTCTCCACAAAGAGAA 848
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US-07-901-703-14

; Sequence 14, Application US/07901703
; Patent No. 5344654
; GENERAL INFORMATION:
; APPLICANT: RUEGER, DAVID C
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZAKAYNAK, ENGIN
; TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: EXCHANGE PLACE, 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07901,703
; FILING DATE: 19920616
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..1196
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "BMP2A"
; OTHER INFORMATION: /note= "BMP2A (CDNA)"
; US-07-901-703-14

Alignment Scores:
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Percent Similarity: 99.75% Conservative: 0
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Query Match: 99.71% Indels: 0
DB: 2 Gaps: 0

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; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..1196
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "CMP2A"
; OTHER INFORMATION: /note= "CMP2A (CDNA)"
US-08-147-023-4

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Pred. No.: 1.01e-199 Length: 1260
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Query Match: 99.71% Indels: 0
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DB 69 GCGGCTGGCCCTGTTCCGGAGCTGGCGCGCAGGAAGTTCCGGCGGCGTCTGTCGGCGC 128
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DB 129 CCCTCATCCAGCCCTCTGACGAGGTCCTGACGAGGTCCTGACGAGTTCGAGTTGCGGCTGCTCAGCATG 188
QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProTyMetLeu 80
DB 189 TTCGGCTGAACAGAGACCCGCCCGCAGGAGCGCGTGGTGGTCCCTCATGCTA 248
QY 81 AspLeuTyArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
DB 249 GACCTGTATCGCAGCAGCTCGGGTCAGCGGGCTCACCGGCCCGCAGACCCCGTTGGAG 308
QY 101 ArgAlaLeuSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
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QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
DB 369 CTACCAAGAACGAGTGGGAAACCAACCGGAGATCTCTTTTAATTTAAGTTCTATCCCC 428
QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
DB 429 ACGGAGGAGTTATCACTCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGTGTCT 488
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QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
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DB 669 CAGCCCAACCATGGATTTCGTGGTGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 728
QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
DB 729 AAGAGACATGTTAGGATAGCAGGTCTTTGACCAACAGATGAACACAGCTGGTTCACATA 788
QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
DB 789 AGCCATTGCTAGTAACTTTTGGCCATGATGTAAGAAAGGCGCATCTCTCCACAAAGAGAA 848
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DB 1089 TGTGTCCCGACAGACTCAGTGTCTATCTCATGCTGTACTTGTACCTTGACGAGATGAAGGTT 1148
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DB 1149 GTATTAAAGAACTATCAGGATATGTTGTGGAGGGTTGTGGGTGTCTGCTGC 1196

RESULT 12
US-08-447-570-4
; Sequence 4, Application US/08447570
; Patent No. 5714589
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,570
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIORITY APPLICATION DATA:
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APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: FITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
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LOCATION: 9..1196
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US-08-447-570-4
Alignment Scores:
Pred. No.: 1,01e-199 Length: 1260
Score: 2092.00 Matches: 395
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Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
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729 AAGAGACATGTTAGGATNAGCAGGTCTTTGACCAAGATGAACACAGCTGGTCACAGATA 788
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 ; Sequence 4, Application US/08449700
 ; Patent No. 5863758
 ; GENERAL INFORMATION:
 ; APPLICANT: OPPERMAN, HERMANN
 ; APPLICANT: OZKAYNAK, ENGIN
 ; APPLICANT: KUBERASAMPATH, THANGAVEL
 ; APPLICANT: RUEGER, DAVID C.
 ; APPLICANT: PANG, ROY H.L.
 ; TITLE OF INVENTION: OSTEOGENIC DEVICES
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
 ; STREET: 53 STATE STREET
 ; CITY: BOSTON
 ; STATE: MASSACHUSETTS
 ; COUNTRY: U.S.A.
 ; ZIP: 02109

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/08/449,700

APPLICATION NUMBER: US 315,342
 FILING DATE: 23-FEB-1989
 PRIOR APPLICATION DATA: US 232,630
 FILING DATE: 15-AUG-1988
 PRIOR APPLICATION DATA: US 179,460
 FILING DATE: 08-APR-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: PITCHER, EDMUND R.
 REGISTRATION NUMBER: 27,829
 REFERENCE/DOCKET NUMBER: CRP-001CP6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/248-7000
 TELEFAX: 617/248-7100
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1260 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: HOMO SAPIENS
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 9..1196 /function= "OSTEOGENIC PROTEIN"
 OTHER INFORMATION: /product= "CBMP2A"
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 US-08-449-700-4

Alignment Scores:
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 Query Match: 99.71% Indels: 0
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 Db 189 TTCGGCCTGAACAGAGACCCACCCCGAGGAGCCCGTGGTGGCCCTCATGCTA 248
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Db 669 CACGCCAACCATGATTCGTGTGGAGTGGAGTGGCCCACTTGGAGGAGAACCAAGGTGTCTCC 728
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Db 1089 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTGACGAGATGAAGAAGTT 1148
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
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RESULT 14

US-08-449-699A-4.
; Sequence 4, Application US/08449699A
; Patent No. 5958441
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKANAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H. L.
; TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,699A
FILING DATE: 24-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023
FILING DATE: 01-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-001CP6CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: CDS /function= "OSTEOGENIC PROTEIN"
LOCATION: 9..1196 /product= "CBMP2A"
OTHER INFORMATION:
OTHER INFORMATION: /note= "CBMP2A (cDNA)"
US-08-449-699A-4

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US-10-801-648-2 (1-396) x US-08-449-699A-4 (1-1260)

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US-09-148-925C-4

; Sequence 4, Application US/09148925C

; Patent No. 6551995

; GENERAL INFORMATION:

; APPLICANT: OPPERMANN, HERMANN

; OZKAYNAK, ENGIN

; KUBERASAMPATH, THANGAVEL

; RUEGER, DAVID C.

; PANG, ROY H.L.

; TITLE OF INVENTION: OSTEOGENIC DEVICES

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

; STREET: 125 HIGH STREET

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: U.S.A.

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/148,925C
FILING DATE: 04-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/148,925
FILING DATE: 8-SEP-1998
APPLICATION NUMBER: US 08/449,699
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: US 08/147,023
FILING DATE: 1-NOV-1993
APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/827,052
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: US 07/579,865
FILING DATE: 7-SEP-1990
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FILING DATE: 4-DEC-1990
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FILING DATE: 4-DEC-1990
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FILING DATE: 20-DEC-1991
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FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 07/600,024
FILING DATE: 18-OCT-1990
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FILING DATE: 18-OCT-1990
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FILING DATE: 21-NOV-1990
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FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
FILING DATE: 08-APR-1988
APPLICATION NUMBER: US 07/232,630
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APPLICATION NUMBER: US 07/315,342
FILING DATE: 23-FEB-1989
APPLICATION NUMBER: US 07/660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,613
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,623
FILING DATE: 17-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: CDS
LOCATION: 9..1196
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "CBMP2a"
/note= "CBMP2(a) (CDNA)"
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US-09-148-925C-4

Alignment Scores:

Pred. No.: 1,01e-199 Length: 1260
Score: 2092.00 Matches: 395
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 1
Query Match: 99.71% Indels: 0
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US-10-801-648-2 (1-396) x US-09-148-925C-4 (1-1260)

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2006, 23:47:24 ; Search time 696 Seconds
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Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA.Main:

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4	2098	100.0	1547	US-10-366-345-10	Sequence 10, Appl
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6	2098	100.0	1547	US-10-302-812-19	Sequence 19, Appl
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36	1269	60.5	1751	7	US-10-240-425-1309	Sequence 1309, Ap
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ALIGNMENTS

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; Publication No. US20020159986A1
; GENERAL INFORMATION:
; APPLICANT: LANGENFELD, John
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF CP
; FILE REFERENCE: 270/0700S
; CURRENT APPLICATION NUMBER: US/10/044,716
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US60/261,252
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US-10-044-716-1

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Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGGCAGCCAGCCGACCCACACTGTGCGCAGCTTCCACCATGAGGATCTTTGGAGAA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCAGAAACGAGTGGGAAACACCCCGGAGATCTCTCTTTAATTTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCACTTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 804 TTAGAAACAATAGCAGTTTCATCACCAGATTATATTAATTAATTAATTAATTAATTAATTA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACTCGAAATTCCTCCGTCGACAGACTTTTGGACACACAGGTTGGTGAATCAGAT 923
Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
Db 924 GCAAGCAGGTGGGAAAGTTTGTATGTCACTCCCGCTGTGTATGCGGTGGACTGCAAGGGA 983
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCAATGGATTCTGTGGTGGAGTGGCCCACTTTGGAGGAGAAACAAAGGTGTCTCC 1043

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Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
Db 1044 AAGAGACATGTTAGGATAAGCAGGCTCTTTGACCAAGATGAACACAGCTGTCACAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTTGCTAGTAACCTTTTGCCCATGTAGGAAGAGGCGATCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAAGCTCAAGCCAAACACACAGCGAAGCGCTTAAGTCCAGCTGTTAAGAGACACCCCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTyrPAsnAspTyrIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTGCAGTGGGCTGGAATGACTGGGATTTGGCTCCCGGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLysLeuAsnSerThr 340
Db 1284 CAGCCCTTTTACTGCCACGAGGAGATGCCCTTTTCTCTGGCTGATCATCTGAACTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 AATCATGCCATTGTTCAGACGTTGGTCAACTCTGTTAACTCTAAGATTCTTAAGGCATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCCGCAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAAATGAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTTGTGGAGGTTTGTGGGTGTCGC 1511

RESULT 2
US-10-286-152A-1
; Sequence 1, Application US/10286152A
; Publication NO. US20030134308A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Research, Ltd.
; TITLE OF INVENTION: Bone Morphogenic Proteins (BMP), BMP Receptors and BMP Binding Pr
; TITLE OF INVENTION: and Their Use in the Diagnosis and Treatment of Glaucoma
; FILE REFERENCE: 2312 US
; CURRENT APPLICATION NUMBER: US/10/286,152A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-286-152A-1

Alignment Scores:
Pred. No.: 8.92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x US-10-286-152A-1 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGGTGGCGGAGCCCGCTGCTTCTAGCGTTGCTTCCCGCAGGCTCTCTCGGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaAlaSerSerGlyArg 40
Db 384 GCGGCTGGCCCTCGTTCGCGAGCTGGCGGCGAGGATTCGCGGCGGCGTCTCGGGCGGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60

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Db 444 CCTCATCCAGCCCTCTGACGAGTCTGAGCGAGTTTCGAGTTTCGGCTGCTCAGCATG 503
QY 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 504 TTCGGCCCTGAACACAGAGACCCACCCCGACGAGGCGCGTGGTCCCGCCCTACATGCTA 563
QY 81 AspLeuTyrArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGACGCACTCAGGTCAGCGGGCTCACCGCGCCAGACACCGGGTTGGAG 623
QY 101 ArgAlaLysArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGGCAGCCAGCGGAGCAACTGTGGCGAGCTTCCACCAATGAAGAATCTTTGGAAGA 683
QY 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerLeuPro 140
Db 684 CTACAGAAACAGTGGGAAACACCCCGGAGATCTCTTAATTTAAGTCTATATCC 743
QY 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATCGAATGCT 803
QY 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db 804 TTAGGAACAATAGCAGTTTCATCACCGAATTAATATTTATGAATCATAAACCTGCA 863
QY 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCAACTCGAAATTCCTCCGTCACAGACTTTTGGACACACAGGTTCGTGAATCAGAA 923
QY 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 924 GCAAGCAGTGGGAAAGTTTGTGTCACCCCGCTGTGTGCGGTGACATGCACAGGGA 983
QY 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCATGGATTCTGTGTGGAAGTGGCCCACTTTGGAGGAAACAGGTGCTCTCC 1043
QY 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
Db 1044 AAGAGACATGTTAGGATAGCAGGCTTTTGGACCAAGATGAACACAGCTGTGTACAGATA 1103
QY 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGCCATCTGTAGTAACTTTTGGCCATGTATGGAAGAGGCATCTCTCCACAAAGAGAA 1163
QY 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAACGTCAAGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAAGACACCT 1223
QY 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGATGATGCTGGATTGTGGCTCCCGGGGTAT 1283
QY 321 HisAlaPheTyrCysHisGlyCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCCCTTTACTGCCAGGAAAGGCCCTTTCTCTGGCTGATCATCTGAACCTCACT 1343
QY 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 ATCATGCAATGTTTCAGACGTTGTCACTCTGTTAACTCTAAGATCTCTTAAGCATGC 1403
QY 361 CysValProThrGluSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCCGACAGAACTCAGTGCTATCTGATGCTGTACCTTGACGAGAAATGAAAGGTT 1463
QY 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG 1511

RESULT 3

US-10-139-814-1

; Sequence 1, Application US/10139814

; Publication No. US20030134790A1
; GENERAL INFORMATION:
; APPLICANT: Langenfeld, John
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 273/136 Michael J. Wise
; CURRENT APPLICATION NUMBER: US/10/139,814
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US60/261,252
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US10/044,716
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1547)
; OTHER INFORMATION: Homo sapiens: Taxon:9606
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1547)
; OTHER INFORMATION: BMP2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (324)..(1514)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (429)..(1127)
; OTHER INFORMATION: Region: TGF-beta propeptide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (432)..(432)
; OTHER INFORMATION: Allele = "T"; Allele = "G"
; FEATURE:
; NAME/KEY: variation
; LOCATION: (584)..(584)
; OTHER INFORMATION: Allele = "A"; Allele = "G"
; FEATURE:
; NAME/KEY: variation
; LOCATION: (893)..(893)
; OTHER INFORMATION: Allele = "T"; Allele = "A"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1209)..(1511)
; OTHER INFORMATION: TGF-beta; Region: Transforming growth factor-beta (TGF-beta) family
; US-10-139-814-1

Alignment Scores:
Pred. No.: 8,92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-801-648-2 (1-396) x US-10-139-814-1 (1-1547)

QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuValLeuLeuGlyGly 20
Db 324 ATGGTGGCGCGGACCCCGCTGCTTCTAGCTTGCTCTCCCGAGTCTCTCTGGCGGC 383
QY 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAsnSerGlyArg 40
Db 384 GCGGCTGGCTCGTTCGGAGCTGGGCGCGAGAGTTTCGGCGCGCTGCTCGGCGCGC 443


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RESULT 4
US-10-366-345-10
; Sequence 10, Application US/10366345
; Publication No. US20030224501A1
; GENERAL INFORMATION:
; APPLICANT: Young, et al.
; TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and
; FILE REFERENCE: PT189
; CURRENT APPLICATION NUMBER: US/10/366,345
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-366-345-10

Alignment Scores:
Pred. No.:      8.92e-227      Length:      1547
Score:          2098.00        Matches:     396
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:     0
Query Match:      100.00%      Indels:      0
DB:               6           Gaps:       0

US-10-801-648-2 (1-396) x US-10-366-345-10 (1-1547)

Qy   1  MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db   324 ATGTTGCGCGGGACCGCTGCTCTTAGCGTTGCTGTTCCCGAGGTCCTCTCTGGGCGGC 383
Qy   21  AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg 40
Db   384 GCGGCTGGCTCGTTTCGGAGCTGGGCGCGAGGAAGTTCCGCGCGCGCTGCTCGCGGCGCG 443
Qy   41  ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db   444 CCTCATCCAGCCCTCTGAGAGGCTCTGAGCGAGTTCGAGGTTGCGGCTGCTCAGCATG 503
Qy   61  PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db   504 TTCGGCTTGAACAGAGACACCCCGGAGGAGCGCGTGGTGCCCTACATGCTA 563
Qy   81  AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db   564 GACCTGTATCGCAGGCACTCAGGTTCAGCGGCTCAGCCGCCAGACCCAGCCGGTTGGAG 623
Qy   101 ArgAlaAlaSerArgAlaAenThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db   624 AGGCGACCGAGCGGAGCAACACACTGTGCGGAGCTTCCACCATGAAGAATCTTTGGAAGA 683
Qy   121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db   684 CTACCAAGAACGAGTGGGAAAACACCCCGGAGATTCCTTTAATTTAAGTTCTATCCCC 743
Qy   141 ThrGluGluPheLeThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db   744 ACGGAGGAGTTTATCACTCAGCTCAGCAGAGCTTTGGACACCGAGCTTTGGTGAATCAGAT 803
Qy   161 LeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAla 180
Db   804 TTAGGAACCAATAGCAGTTTCCATCCGGAATTAATATTATGAAATCATATAAACCTGCA 863
Qy   181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db   864 ACAGCCAACTCGAAATTCCTCCGTGACAGACTTTTGGACACCGAGCTTTGGTGAATCAGAT 923
Qy   201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db   924 GCAAGCAGTGGGAAAGTTTGTATGTACCCCGCTGTGATCGGTGGACTGTGCACAGGGA 983
Qy   221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db   984 CACGCCAACCAATGATTCGTGGTGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
Qy   241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db   1044 AAGAGACATGTTAGATTAAGCAGCTCTTTCACCAAGATGAACAGCTGGTACAGATA 1103
Qy   261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db   1104 AGGCCATTGTCTAGTAACCTTTTGGCCATGATGSAAGAGGCACTCTCTCCACAAAGAGAA 1163
Qy   281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db   1164 AACGTCAGCCAAACAAACACGCGGAACGCTTAAAGTCAGCTGTAGAGACACCCCT 1223
Qy   301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyr 320
Db   1224 TTGTACGTGGACTTCAGTACGTGGGTGGAAATGACTGGATTTGTGGCTTCCCGGGGTAT 1283
Qy   321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db   1284 CACGCCCTTTACTGCCACGAGAAATGCCCTTTCTCTGGCTGATCATCTGAACTCCACT 1343
Qy   341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db   1344 AATCATGCCATTGTTCAGACGTGGTCAACTCTGTAACTCTAAGATTCTCTAAGGCAATGC 1403
Qy   361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db   1404 TGTGTCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTTGACGAGATGAAGAGTT 1463
Qy   381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db   1464 GTATTAAAGAACTATCAGGACATGCTGTGGAGGGTTGTGGGTGTGCTGCG 1511
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Qy	221	HisAla	AsnHis	GlyPhe	ValVal	GluVal	AlaHis	LeuGlu	LeuGly	ValSer	240	
Db	984	CAGCC	AACAT	TGAT	TCGT	TGGT	TGAAG	TGCCCC	CACCT	TTCGAG	GAGAAACAAGGT	1043
Qy	241	LysArg	HisVal	ArgIle	SerArg	SerLeu	HisGln	AspGlu	HisSer	TrpSer	GlnIle	260
Db	1044	AAGAG	ACAT	TGT	TAGG	ATAC	CGATCT	TTTGC	ACCAC	AGATGAAC	CACAGCTGGT	1103
Qy	261	ArgPro	LeuLeu	ValThr	PheGly	HisAsp	GlyLys	GlyHis	ProLeu	HisLys	ArgGlu	280
Db	1104	AGGCC	ATTC	TGT	TAAC	TTTTT	TGGC	ATGATG	GAAGAAG	GGCATCTCT	TCCACAA	1163
Qy	281	LysArg	GlnAla	LysHis	LysGln	ArgLys	ArgLeu	LysSer	SerCys	LysArg	HisPro	300
Db	1164	AAAGT	CAAGC	CAAC	CAAC	ACGCG	GAAC	CGCCT	TAA	GTC	CTGTAAGAG	1223
Qy	301	LeuTyr	ValAsp	PheSer	AspVal	GlyTyr	ProAsn	AspTrp	IleVal	AlaPro	ProGly	320
Db	1224	TTGT	AC	TGG	AC	TTT	CAGT	CGCT	CGGGT	TGGAAT	CAC	1283
Qy	321	HisAla	PheTyr	CysHis	GlyGly	CysPro	PhePro	LeuAla	AspHis	LeuAsn	SerThr	340
Db	1284	CACGC	CTTT	TACT	CCCA	CGGAGA	TG	CCCTTT	CCTCT	TGGCT	GAATCAT	1343
Qy	341	AsnHis	AlaIle	ValGln	ThrLeu	ValAsn	SerVal	AsnSer	LysIle	ProLys	AlaCys	360
Db	1344	AATCAT	TGCC	ATT	GTTC	AG	CGTT	TGGT	TAAC	TCTCT	GTAACT	1403
Qy	361	CysVal	ProThr	GluLeu	SerAla	IleSer	MetLeu	TyrLeu	AspGlu	AsnGlu	LysVal	380
Db	1404	TGTGT	CCCG	CAG	AACT	CAGT	GTCT	ATCT	CGAT	GTCT	GTACCT	1463
Qy	381	ValLeu	LysAsn	TyrGln	AspMet	ValVal	GluGly	CysGly	CysArg			396
Db	1464	GTA	TTAA	GAAC	TAT	CAG	CA	TGGT	TCT	TG	GAGG	1511

RESULT 5

US-10-295-027-159
Sequence 159, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Nataasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynnne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250

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; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 159
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-159

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Alignment Scores:				
Pred. No.:	8-92e-227	Length:	1547	
Score:	2098.00	Matches:	396	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	6	Gaps:	0	
US-10-801-648-2 (1-396) x US-10-295-027-159 (1-1547)				
Qy	1	MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly	20	
Db	324	ATGGTGGCGGGACCCGCTGTCTTTAGGGTGTCTGTCTCCACAGGTCTCTCTGGGGCGC	383	
Qy	21	AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg	40	
Db	384	GCGGCTGGCTGTTCCGGAGCTGGGCGCAGAGATTCCGGCGCGTGTGTGGCGCGC	443	
Qy	41	ProSerSerGlnProSerSerGluValLeuSerGluPheGluLeuArgLeuLeuSerMet	50	
Db	444	CCCTCATCCAGCCCTCTGACGAGGTCTTGGAGCGAGTTCGAGTTCGGGTGTCTCAGCATG	503	
Qy	61	PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu	80	
Db	504	TTGGGGCTGAAACAGAGACCCACCCCGAGGAGCGCGTGGTGCCTTACATGCTA	563	
Qy	81	AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu	100	
Db	564	GACCTGTATCGCAGGCACTCAGTTCAGCGGGCTCACCCGCCAGACCACCGTTGGAG	623	
Qy	101	ArgAlaAlaSerArgAlaIleThrValArgSerPheHisHisGluSerLeuGluGlu	120	
Db	624	AGGCGACCCAGCCGAGCAACACTGTGTGGCAGCTTCCACCATGAGAAATCTTTGGAGAA	683	
Qy	121	LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro	140	
Db	684	CTACCAAAACGAGTGGGAAACACCCGAGAGATCTCTTTAATTTAATTTATATCTTCCC	743	
Qy	141	ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla	160	
Db	744	ACGGAGGGTTTATCACCTCAGCAGAGCTTCAGGTTTTCCGAGAACAGATGCAAGATGCT	803	
Qy	161	LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla	180	
Db	804	TTAGGAAACATAGCAGTTCCTCATCCGAAATTAATTTATGAAATCTATAAAACCTGCA	863	
Qy	181	ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn	200	
Db	864	ACAGCCAACTCGAAATTTCCCGTGGACAGAGCTTTTGGACACACAGGTTGGTGAATCAGAT	923	
Qy	201	AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly	220	
Db	924	GCAAGCAGTGGGNAAGTTTGTATGTTCACCCCGCTGTGTATGGGTGGAGTCGCACAGGGA	983	
Qy	221	HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer	240	
Db	984	CACGCCAACCATGATTTCGTGGTGGAAAGTGGCCCACTTTGGAGGAGAGAAACAGGTGTCTCC	1043	
Qy	241	LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle	260	
Db	1044	AAGAGACATGTTAGGATPAGCAGGTCTTTGCCACAGATGAACACAGCTGTGTACACAGATA	1103	

Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db 1104 AGGCATTCGTAGTAACCTTTTGGCCATGATGGAAGGGGCATCTCTCCACAAAGAGAA 1163
 Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 Db 1164 AAACGTCAAGCAACACAAACAGCGGAAAGCCCTTAAGTCCAGCTGTAGAGACACCT 1223
 Qy 301 LeuTyrValAspPheSerAspValGlyTyrPheAspTrpIleValAlaProProGlyTyr 320
 Db 1224 TTGTACGTGGACTTCAGTACGTGGGTGGAATGACTGGATGTGGCTCCCGGGGTAT 1283
 Qy 321 HisAlaPheTyrCysHisGlyGlyCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db 1284 CACGCCCTTTACTGCCACGGAGATGCCCTTTCTCTGGCTGATCATCTGAATCCACT 1343
 Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 Db 1344 AATCATGCCATTGTTACAGCGTTGGTCACTCTGTAACTTAAGATTCCTAAGGCATGC 1403
 Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 Db 1404 TGTGTCCCGACAGAACTCAGTGTCTCTCGATGCTGTACCTTGACGAGATGAAGAGTT 1463
 Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluCysGlyCysArg 396
 Db 1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG 1511

RESULT 6

US-10-302-812-19
 ; Sequence 19, Application US/10302812
 ; Publication No. US20040087016A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Keating et al.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DIFFERENTIATION AND
 ; TISSUE REGENERATION
 ; FILE REFERENCE: HYDR-P02-004
 ; CURRENT APPLICATION NUMBER: US/10/302,812
 ; CURRENT FILING DATE: 2002-11-21
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 19
 ; LENGTH: 1547
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-302-812-19

Alignment Scores:

Pred. No.: 8.92e-227 Length: 1547
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-801-648-2 (1-396) x US-10-302-812-19 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
 Db 324 ATGGTGGCGGGAGCCCGCTGTCTTCTAGCGTTGCTGCTTCCCGAGGTCTCTCTGGCGGC 383
 Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaIleSerSerGlyArg 40
 Db 384 CGCGCTGGCTCGTTCCGAGCTGGCGCGAGGTTCCGCGCGCGGTCTCGTGGCGCGC 443
 Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 Db 444 CCTCATCCAGCCCTCTGACAGGTCTGACGAGTTCCAGTTGCGGCTGCTCAGCATG 503
 Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
 Db 504 TTGGGCTGAAACAGAGACCCACCCCGAGCGGACCGCGTGTGGTGTGCCCCCTACATCTA 563

Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db 564 GACCTGTATCGCAGGCACTCAGGTCAAGCGGGCTACCCCGCCAGACCAACCGGTTGGAG 623
 Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGluGlu 120
 Db 624 AGGCGACCGACCGAGCAACACTGTGCGCAGCTTCCACCATGAAGAAATCTTTGGAAGAA 683
 Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
 Db 684 CTACCAGAAACGAGTGGGAAAAACAACCCGGAGATTCTCTTTAATTTAAGTTCTATCCCC 743
 Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 Db 744 ACGGAGGAGTTTATCATCCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 803
 Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla 180
 Db 804 TTAGGAACAATAGCAGTTTCCATCCCGAATTAATATTATGAATCATAAACCTTGCA 863
 Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 Db 864 ACAGCCAACCTCGAAATTTCCCGGTGACCAGACTTTTGGACACCAAGTTGGTGAATCAGAAT 923
 Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
 Db 924 GCAAGCAGGTGGGAAAGTTTGTATGTCAACCCCGCTGTGTATGCGGTGAGATGCACAGGA 983
 Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
 Db 984 CACGCCAACCATGGATTGCTGGTGGAGTGGCCCACTTGGAGGAGAAACAGGTGTCTCC 1043
 Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 Db 1044 AAGAGACATGTTAGGATAAGCAGTCTTTGCCAACAGATGAACACACAGCTGTGTACAGATA 1103
 Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db 1104 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGGGGCATCTCTCCACAAAGAGAA 1163
 Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 Db 1164 AAACGTCAAGCAACACAAACAGCGGAAAGCCCTTAAGTCCAGCTGTAGAGACACCT 1223
 Qy 301 LeuTyrValAspPheSerAspValGlyTyrPheAspTrpIleValAlaProProGlyTyr 320
 Db 1224 TTGTACGTGACTTCAGTACGTGGGTGGAATGACTGGATTTGTGGCTCCCGGGGTAT 1283
 Qy 321 HisAlaPheTyrCysHisGlyGlyCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db 1284 CACGCCCTTTACTGCCACGGAGATGCCCTTTCTCTGGCTGATCATCTGAATCCACT 1343
 Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 Db 1344 AATCATGCCATTGTTACAGCTTGGTCACTCTGTAACTTCTAAGATTCCTAAGGCATGC 1403
 Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 Db 1404 TGTGTCCCGACAGAACTCAGTGTCTCTCGATGCTGTACCTTGACGAGATGAAGAGTT 1463
 Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluCysGlyCysArg 396
 Db 1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG 1511

RESULT 7

US-10-283-975A-403
 ; Sequence 403, Application US/10283975A
 ; Publication No. US20040110792A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ortho-Clinical Diagnostics, Inc.
 ; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
 ; FILE REFERENCE: CDS 293 PCT

;; CURRENT APPLICATION NUMBER: US/10/283,975A
;; CURRENT FILING DATE: 2002-10-30
;; PRIOR APPLICATION NUMBER: 60/340,938
;; PRIOR FILING DATE: 2001-10-30
;; PRIOR APPLICATION NUMBER: 60/338,997
;; PRIOR FILING DATE: 2001-10-30
;; PRIOR APPLICATION NUMBER: 60/340,081
;; PRIOR FILING DATE: 2001-10-30
;; PRIOR APPLICATION NUMBER: 60/341,012
;; PRIOR FILING DATE: 2001-10-30
;; NUMBER OF SEQ ID NOS: 900
;; SOFTWARE: Patent in version 3.1
;; SEQ ID NO 403
;; LENGTH: 1547
;; TYPE: DNA
;; ORGANISM: HUMAN
US-10-283-975A-403

Alignment Scores:
Pred. No.: 8,92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-801-648-2 (1-396) x US-10-283-975A-403 (1-1547)

Qy	1	MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly	20
Db	324	ATGTTGGCGGGACCCGCTTCTAGCGTTGCTTCCAGGTCCTCTCGGGGCGC	383
Qy	21	AlaAlaGlyLeuValProGluLeuGlyArgArgGlyPheAlaAlaAAserSerGlyArg	40
Db	384	CGCGCTGGCCCTCGTTCCGGAGCTGGCGCGCGAGAGTTCCGCGCGCGCGC	443
Qy	41	ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuLeuLeuSerMet	60
Db	444	CCCTCATCCAGCCCTCTGACGAGTCTTGACGAGTTCCGAGTTGCGGCTGCTCAGCATG	503
Qy	61	PheGlyLeuLeuGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu	80
Db	504	TTGGGCTGTAACAGAGACCCACCCAGCAGGAGCGCGTGGTGGCCCTTACATGCTA	563
Qy	81	AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu	100
Db	564	GACCTGTATCGCAGCACTCAGGTGAGCGCGGCTCACCGCGCCAGACACCGGTTGAG	623
Qy	101	ArgAlaAAserArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu	120
Db	624	AGGGCAGCCAGCCGAGCCCAACTGTGCGCAGCTTCCACCATGAAGAATCTTTGGAAGA	683
Qy	121	LeuProGluThrSerGlyLeuThrArgArgPhePheAsnLeuSerSerIlePro	140
Db	684	CTACAGAAACGAGTGGGAAACACCCGAGATCTCTTTAATTAAATTCATCCCTCC	743
Qy	141	ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla	160
Db	744	ACGGAGGAGTTTATCACTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT	803
Qy	161	LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleIleIleIle	180
Db	804	TTAGGAAACAAATAGCAGTTTCATCACCAGATTAATATTTATGAATCATAAACCTGCA	863
Qy	181	ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn	200
Db	864	ACAGCAACTCGAAATTCCTCCGTGACAGACTTTTGGACACAGGTTTGGTGNATCAGAT	923
Qy	201	AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly	220
Db	924	GCAAGCAGGTGGGAAAGTTTTCATGTACCCCGCTGTGATGCGGTGACATGCACAGGGA	983
Qy	221	HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluIleGlnGlyValSer	240

Db	984	CACGCCAACCATGATTGCTGGTGGAAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC	1043
Qy	241	LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle	260
Db	1044	AAGAGCATGTTAGATAGCAGGTCTTTGCCACAGATGACACAGCTGGTCTACAGATA	1103
Qy	261	ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu	280
Db	1104	AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAGAGGCGATCTCTCCACAAAGAGAA	1163
Qy	281	LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro	300
Db	1164	AAACGTCAAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTGAAGAGACACCT	1223
Qy	301	LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr	320
Db	1224	TTGTACGTGGACTTCAGTGACGTGGGTGGAATGACTGGATTTGGCTTCCCGGGGTAT	1283
Qy	321	HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr	340
Db	1284	CACGCCTTTACTGCCACGAGGAGATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT	1343
Qy	341	AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys	360
Db	1344	AATCATGCCATTGTTCAAGCGTTGGTCAACTCTCTTAAGTCTTAAGATTTCTTAAGGCATGC	1403
Qy	361	CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluIleVal	380
Db	1404	TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGACCTTGACGAGAAATGAAAAGTT	1463
Qy	381	ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg	396
Db	1464	GTATTAAGAAGTAATCAGACATGTTGTGGAGGTTGTGGGTGTGCG	1511

RESULT 8

US-10-692-824-1
; Sequence 1, Application US/10692824
; Publication No. US20040126375A1
; GENERAL INFORMATION:
; APPLICANT: Langenfeld, John
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 54704, 8036, US03
; CURRENT APPLICATION NUMBER: US/10/692,824
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US60/261,252
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US10/044,716
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1547)
; OTHER INFORMATION: Homo sapiens: Taxon:9606
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1547)
; OTHER INFORMATION: BMP2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (324)..(1514)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (429)..(1127)
; OTHER INFORMATION: Region: TGF-beta propeptide
; FEATURE:
; NAME/KEY: variation

	/	LOCATION:	(432)..(432)	
	/	OTHER INFORMATION:	Allele = "T"; Allele = "G"	
	/	FEATURE:		
	/	NAME/KEY:	variation	
	/	LOCATION:	(584)..(584)	
	/	OTHER INFORMATION:	Allele = "A"; Allele = "G"	
	/	FEATURES:		
	/	NAME/KEY:	variation	
	/	LOCATION:	(893)..(893)	
	/	OTHER INFORMATION:	Allele = "T"; Allele = "A"	
	/	FEATURE:		
	/	NAME/KEY:	misc feature	
	/	LOCATION:	(1209)..(1511)	
	/	OTHER INFORMATION:	TGF-beta; Region: Transforming growth factor beta like domain	
	/	FEATURES:		
	/	NAME/KEY:	misc feature	
	/	LOCATION:	(1209)..(1511)	
	/	OTHER INFORMATION:	TGFB; Region: Transforming growth factor-beta (TGF-beta) family	
	/	US-10-692-824-1		
		Alignment Scores:		
		Pred. No.:	8.92e-227	Length: 1547
		Score:	2098.00	Matches: 396
		Percent Similarity:	100.00%	Conservative: 0
		Best Local Similarity:	100.00%	Mismatches: 0
		Query Match:	100.00%	Indels: 0
		DB:	7	Gaps: 0
		US-10-801-648-2 (1-396) x US-10-692-824-1 (1-1547)		
Qy		1	MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGly	20
Db		324	ATGGTGCGCGAGCCGCTGTCTTAGCGTTGCTGTCCACAGTCCTCTGGCGGC	383
Qy		21	AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArg	40
Db		384	CGCGCTGCGCTCGTTCGAGACTGGGCCGAGAGAATTTCGCGCGCGCTCGTCGCGCGC	443
Qy		41	ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet	60
Db		444	CCCTCATCCAGCCCTCTGACGAGGTCTCTGACGAGTTCTCGAGTTGCGGCTGCTCAGCA	503
Qy		61	PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProFyrMetLeu	80
Db		504	TTCGGCTGAACAACAGAGACCACCCCAAGAGGACGGTGTGTCGCCCTTACATGCTA	563
Qy		81	AspLeuYrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu	100
Db		564	GACCTGTATCCAGCGCACTCAGGTGAGCGGGCTCACCGCGGCCACACCGGTTGGAG	623
Qy		101	ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu	120
Db		624	AGGCGAGCCAGCCAGCCAACTGTGCGAGCTTCCACCATGAAGAATCTTTGAAGAA	683
Qy		121	LeuProGluThrSerSerGlyLeuThrThrArgArgPhePheAsnLeuSerSerIlePro	140
Db		684	CTACCAGAAAACAGTGGGAAAAACAACCCGGAGATCTCTTTTAATTTAAGTTCTATCCC	743
Qy		141	ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla	160
Db		744	ACGAGAGATTTATCACCTCAGCAGAGCTTCAGGTTTTCCGAGAACAGATGCAAGATGCT	803
Qy		161	LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleIysProAla	180
Db		804	TTAGGAACAATAGCAGTTTCCATCCGAATTAATAATTTATGAATCATAAAAACCTGCA	863
Qy		181	ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn	200
Db		864	ACAGCCAATCGAAATTCCTCCGTTGACCAAGCTTTTGGACACCAAGTTGGTGAATCAGAT	923
Qy		201	AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly	220
Db		924	GCAAGCAGTGGGAAAGATTTTGATGTACCCCGCTGTGATCGCGTGAATGCAAGGGA	983

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGGTGGCCGGGACCCCGCTGCTTCTAGCGTTGCTGCTTCCCGAGGCTCTCTGGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
Db 384 CGCGCTGGCCCTCGTTCCGAGCTGGCGCGCAGGAAGTTTCGCGGGCGGCTCGTCCGGCGGC 443
Qy 41 ProSerSerGlnProSerArgGluValLeuSerGluPheGluLeuArgLeuSerMet 60
Db 444 CCTCATCCCCAGCCCTCTGAGCAGGTCTGAGCAGGTTTCGAGTTGCGGCTCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 504 TTCGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGGTGGTCCCTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGCAGCACTCAGGTCAGCGCGGCTCACCAGCCGCCAGACACCGGTTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGGCAGCAGCCGAGCCAACTGTGCGCAGCTTCCACCATGAGAAATCTTTGGAAGAA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCGAACAACGAGTGGGAAACACCCCGGAGATCTTCTTTAATTTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleysProAla 180
Db 804 TTAGGAACAATAGCAGTTTCATCACCGAATTAATATTTATGAATCATATAAACCTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACTCGAAATTCCTGAGCAGACTTTTGGACACGAGTTGGTGGATCAGAT 923
Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
Db 924 GCAACGAGTGGGAAAGTTTGTATGTACCCCGCTGTGTATGCGGTGACTGCACAGGGA 983
Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCATGATTCGTGGTGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTTPSerGlnIle 260
Db 1044 AAGAGACATGTTAGGATAGCAGGCTTTTGGCCATGATGAAAGGCGATCTCTCCACAAAGAGAA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTGCTAGTAATCTTTGGCCATGATGAAAGGCGATCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAACGTCACGCCAAACACAAACAGCGGAAACGCCCTTAAGTCCAGCTGTAAGAGACACCCCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTTPileValAlaProProGlyTyr 320
Db 1224 TTGTAGCTGGATCTCAGTGACGTGGGTGGATGATGATGATGATGATGATGATGATGATGAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CAGCGCTTTTATCTGCCAGGAGATGCCCTTTTCTCTGCTGATCATCTGAATCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 AATCATGCCATTGTTTCAGACGTTGGTCAACTCTGTAACTCTTAAGATTCCTAAGCGATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380

Db 1404 TGTGTCCCGCAGAACTCAGTGTCTATCTCGATGCTGTACCTTCACGAGAATGAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGC 1511
RESULT 10
US-10-489-740-36
; Sequence 36, Application US/10489740
; Publication No. US20050112574A1
; GENERAL INFORMATION:
; APPLICANT: Biomimetics Limited
; TITLE OF INVENTION: P9
; FILE REFERENCE: Angiogenesis PCT
; CURRENT APPLICATION NUMBER: US/10/489,740
; CURRENT FILING DATE: 2004-03-15
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-489-740-36
Alignment Scores:
Pred. No.: 8,92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-801-648-2 (1-396) x US-10-489-740-36 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGGTGGCCGGGACCCCGCTGCTTCTAGCGTTGCTGCTTCCCGAGGCTCTCTGGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGlyArg 40
Db 384 CGCGCTGGCCCTCGTTCCGAGCTGGCGCGCAGGAAGTTTCGCGGGCGGCTCGTCCGGCGGC 443
Qy 41 ProSerSerGlnProSerArgGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCCCCAGCCCTCTGAGCAGGCTCTGAGCGAGTTTCGAGTTGCGGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 504 TTCGGCTGAAACAGAGACCCACCCAGCAGGAGCGCGTGGTGGTCCCTTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGCAGCACTCAGGTCAGCGCGGCTCACCAGCCGCCAGACACCGGTTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGGCAGCAGCCGAGCCAACTGTGCGCAGCTTCCACCATGAGAAATCTTTGGAAGAA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCGAACAACGAGTGGGAAACACCCCGGAGATCTTCTTTAATTTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 803
Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleysProAla 180
Db 804 TTAGGAACAATAGCAGTTTCATCACCGAATTAATATTTATGAATCATATAAACCTGCA 863
Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200


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Db      864 ACAGCCAACTCGAAATTCCTGACAGACTTTTGGACACAGCGTTGGTGAATCAGAAT  923
Qy      201 AlaserArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly  220
Db      924 GCAAGCAGGTGGGAAAGTTTGGATGTACCCCGCTGTGATGCGGTGGACTGCAACAGGGA  983
Qy      221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer  240
Db      984 CACGCCAACCATGGATTCTGTGGTGGAGTGGCCACACTTGGAGGAGAAACAAGTGTCTCC  1043
Qy      241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle  260
Db      1044 AAGACACATGTTAGGATAAGCAGGTCTTTGACCAAGATGAACACAGCTGCTGCACAGATA  1103
Qy      261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu  280
Db      1104 AGGCCATTGCTAGTAACTTTTGGCCATGATGGAAGAGGCGCATCTCTCCACAAAGAGAA  1163
Qy      281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysLysArgHisPro  300
Db      1164 AAACGTCACAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGATTCCTTAAGGATGC  1223
Qy      301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTrpIleValAlaProProGlyTyr  320
Db      1224 TTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACTTGGATTTGGCTCCCGGGGTAT  1283
Qy      321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr  340
Db      1284 CACGCTTTTACTGCGACGCGAGAAATGCCCTTTTCTCTGGCTGATCATCTGACTCCACT  1343
Qy      341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys  360
Db      1344 AATCATGCCATTGTTACAGCGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC  1403
Qy      361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal  380
Db      1404 TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGTACCTTTGACGAGAAATGAAAGGTT  1463
Qy      381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg  396
Db      1464 GTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG  1511

RESULT 11
US-10-492-380-1
; Sequence 1, Application US/10492380
; Publication No. US20050118585A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Research, Ltd.
; TITLE OF INVENTION: Bone Morphogenic Proteins (BMP), BMP Receptors and BMP Binding
; TITLE OF INVENTION: Proteins and their Use in the Diagnosis and Treatment of Glaucoma
; FILE REFERENCE: 2312 US
; CURRENT APPLICATION NUMBER: US/10/492,380
; CURRENT FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-492-380-1

Alignment Scores:
Pred. No.:      8,92e-227      Length:      1547
Score:          2098.00      Matches:      396
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              9          Gaps:      0

US-10-801-648-2 (1-396) x US-10-492-380-1 (1-1547)
Qy      1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly  20
```

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Db      324 ATGTTGCGCGGGACCCCGCTGCTCTCTAGCGTTGCTGCTCTCCACAGGTCCTCTCTGGGCGGC  383
Qy      21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLaserSerGlyArg  40
Db      384 GCGGCTGGCTCGTTCCGAGCTGGGCGCGCAGGAAGTTTCGCGGCGGCTGCTCGGGCGGC  443
Qy      41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet  60
Db      444 CCCTCATCTCCAGCCCTCTGACGAGGCTCTGACGAGTTCGAGTTGCGGCTGCTCAGCATG  503
Qy      61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu  80
Db      504 TTGCGCTGAAACAGAGACCCACCCCGCAGGAGCGCGCTGGTGCCCCCTCATGCTA  563
Qy      81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu  100
Db      564 GACCTGTATCGAGGCACTCAGGTTCAGCGGGCTCACCCGCCCGCAGACCCCGGTGGAG  623
Qy      101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu  120
Db      624 AGGCACGCCAGCGGAGCCAACTGTGCGCAGCTTCCACCATGAAGAATCTTTTGGAGAA  683
Qy      121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro  140
Db      684 CTACCAGAAACGAGTGGGAAACAAACCCGGAGATTCTCTTTAATTTAAGTTCTATCCCC  743
Qy      141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla  160
Db      744 ACGGAGGAGTTTATCCTCCTCAGCAGAGCTTCAGGTTTTCCGAGAACAGATGCAAGATGCT  803
Qy      161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAla  180
Db      804 TTAGGAAACAAATAGCAGTTTCCATCACCGAATTAATAATTTATGAATCATAAAACTGCA  863
Qy      181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn  200
Db      864 ACAGCCAACTCGAAATTTCCCGTGACACAGACTTTTGGACACAGGTTGGTGAATCAGAA  923
Qy      201 AlaserArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly  220
Db      924 GCAAGCAGGTGGGAAAGTTTGGATGTCAACCCCGCTGTGATGCGGTGGACTGCAACAGGA  983
Qy      221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer  240
Db      984 CACGCCAAACCATGGATTCTGTGGTGGAGTGGCGCCACTTGGAGGAGAAACAAGTGTCTCC  1043
Qy      241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle  260
Db      1044 AAGACACATGTTAGGATAAGCAGGTCTTTGACCAAGATGAACACAGCTGCTGCACAGATA  1103
Qy      261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu  280
Db      1104 AGGCCATTGCTAGTAACTTTTGGCCATGATGGAAGAGGCGCATCTCTCCACAAAGAGAA  1163
Qy      281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysLysArgHisPro  300
Db      1164 AAACGTCACAGCCAAACACAAACAGCGGAAACGCTTAAAGTCCAGATTCCTTAAGGATGC  1223
Qy      301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTrpIleValAlaProProGlyTyr  320
Db      1224 TTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACTTGGATTTGGCTCCCGGGGTAT  1283
Qy      321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr  340
Db      1284 CACGCTTTTACTGCGACGCGAGAAATGCCCTTTTCTCTGGCTGATCATCTGACTCCACT  1343
Qy      341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys  360
Db      1344 AATCATGCCATTGTTACAGCGTTGGTCAACTCTGTAACTCTAAGATTCTTAAGGCATGC  1403
Qy      361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal  380
```


Db 1404 TGTGTCCGACAGAACTCAGTCTATCTCGATGCTGTGACCTTGCAGAGAAATGAAAAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTCGC 1511

RESULT 12

US-10-917-265-1

; Sequence 1, Application US/10917265
; Publication No. US20050136042A1
; GENERAL INFORMATION:
; APPLICANT: BETZ, OLIVER B.
; APPLICANT: EVANS, CHRISTOPHER H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TISSUE REPAIR
; FILE REFERENCE: BWY-004.01
; CURRENT APPLICATION NUMBER: US/10/917,265
; CURRENT FILING DATE: 2004-08-11
; PRIOR APPLICATION NUMBER: 60/494,484
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-917-265-1

Alignment Scores:
Pred. No.: 8,92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-801-648-2 (1-396) x US-10-917-265-1 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyCly 20
Db 324 ATGTGTGGCGGACCGCTGTCTTCTAGCGTTGCTGTCCCGAGGTCCTCTGTGGCGGC 383
Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAspSerGlyArg 40
Db 384 GCGGCTGGCGCTCGTTCGAGAGTGGCGCCAGAGAGTTCCGCGCGCGCTGTCGGCGCGC 443
Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
Db 444 CCTCATCCAGCCCTCTGACGAGTCTCTGACGAGTCTGAGCGAGTTCGAGTTCGCGCTGCTCAGCATG 503
Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrMetLeu 80
Db 504 TTCGGCCTGAACAGACAGACCCACCCGACGAGCGCGTGTGTCGCCCTTACATGCTA 563
Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCGCAGGACACTCAGTCAGCGGGCTCACCGCCCGACAGACCCCGTTGGAG 623
Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGlu 120
Db 624 AGGGCAGCAGCGGAGCCCACTGTGCGCAGTTCACCATGAAGATCTTTGGAGAA 683
Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACCAAGAACAGTGGGAAACACCCGAGATCTCTTTAAATTAAGTTCTATCCCC 743
Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCATCCTCAGCAGGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 803
Qy 161 LeuGlyAsnAspSerSerPheHisHisArgGlnIleLeuLeuLeuLeuLeuProAla 180
Db 804 TTAGGAACAATAGCAGGTTTCCATCCGAATTAATTTATTTGAAATCATAAACCTGCA 863

Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAACCTCGAAATTCCTCCGTCGACAGACTTTTGGACACACAGGTTGGTGAATCAGAA 923
Qy 201 AlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGly 220
Db 924 GCAAGCAGGTGGGAAAGTTTGTATGTACCCCCCTGTGATGCGGTGACATGCAACAGGA 983
Qy 221 HisAlaAsnHisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCATGATTCGTGTGGAAGTGGCCCACTTGGAGGAGAAACAGAGTGTCTCC 1043
Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSerGlnIle 260
Db 1044 AAGAGACATGTTAGGTAAGCAGGCTCTTTCACCAAGATGAACACAGCTGCTGCACAGATA 1103
Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATTGCTAGTAACCTTTTGGCCATGATGAAAGGGCATCTCTCTCCACAAAGAGAA 1163
Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AACGTCAGCCAAACACAAACAGCGGAACGCTTAACTCCAGCTGTAAAGAGACACCT 1223
Qy 301 LeuTyrValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTGAGTGGGTGGAATGACTGATGTGTGGTCTCCCGGGGTAT 1283
Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCTTTTACTGCCAGGAGAAATGCCCCCTTTTCTCTGGCTGATCATCTGAACCTCCACT 1343
Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
Db 1344 AATCATGCCATTGTTCAGACGTTGGTCAACTCTGTAACTCTAGATTCTTAAGCAATGC 1403
Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCGACAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGATGAAAGGTT 1463
Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTCGC 1511

RESULT 13

US-10-886-947-1
; Sequence 1, Application US/10886947
; Publication No. US20050197304A1
; GENERAL INFORMATION:
; APPLICANT: New York University School of Medicine
; APPLICANT: Dicesare, Paul
; TITLE OF INVENTION: Nucleic Acid Therapy To Enhance Cartilage Repair
; FILE REFERENCE: 1049-1-037N
; CURRENT APPLICATION NUMBER: US/10/886,947
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,669
; PRIOR FILING DATE: 2003-07-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-886-947-1

Alignment Scores:
Pred. No.: 8,92e-227 Length: 1547
Score: 2098.00 Matches: 396
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-801-648-2 (1-396) x US-10-886-947-1 (1-1547)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 324 ATGGTGGCGGAGCCCGCTGCTTCTAGCGTTGCTGCTTCCCGAGGTCCTCTCGGGCGGC 383

Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlySerPheAlaAlaAspSerSerGlyArg 40
Db 384 GCGGCTGGCTTCGTCGAGCTGGCGCGCAGGAGTTTCGGCGCGGCTGCTCGGGCGGC 443

Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuLeuArgLeuSerMet 60
Db 444 CCCTCATCCAGCCCTCTGACAGAGTCTGAGCGAGTTGAGTTGCGGCTGCTCAGCATG 503

Qy 61 PheGlyLeuValGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
Db 504 TTCGGCTGMAAACAGAGACCACCCAGCAGGAGCGCGTGGTGGCCCCCTACATGCTA 563

Qy 81 AspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
Db 564 GACCTGTATCCAGGCTCTGAGCGAGTCTGAGCGAGTTGAGTTGCGGCTGCTCAGCATG 623

Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
Db 624 AGGCGAGCCAGCGAGCCAACTGTGCGAGCTTCCACCATGAAGATCTTTGGAAGAA 683

Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
Db 684 CTACAGAAACGAGTGGGMAAACCAACCGGAGATCTCTTTAATTTAAGTTCTATCCCC 743

Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
Db 744 ACGGAGGAGTTTATCACTTCAGCAGAGCTTCAGGTTTCGAGAACAGATGCAAGATGCT 803

Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleLysProAla 180
Db 804 TTAGGAACAATAGCATGTTTCATACCGAATTATATATATGAATCATATAAACCTGCA 863

Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
Db 864 ACAGCCAATCGAAATCCCGCTGACCAAGATCTTTTGGACACACAGGTTGGTGAATCAGAT 923

Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
Db 924 GCAAGCAGGTGGGAAAGTTTGTATGTACCCCGCTGTGTATGCGGTGAGCTGCACAGGA 983

Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
Db 984 CACGCCAACCATGGATTGCTGGTGGAGTGGCCCACTTGGAGGAGAAACAGGTTGCTTCC 1043

Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
Db 1044 AAGAGACATGTTAGGATAAGCAGTCTTTTGACCAAGATGAACACAGCTGGTCAAGATA 1103

Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
Db 1104 AGGCCATGTGCTAGTAACCTTTTGGCCATGATGAAAGGCGCATCTCTCCACAAAGAGAA 1163

Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
Db 1164 AAAGCTCAGCCAAACACAAACACGCGGAACCGCTTAAGTCCAGCTGTAGAGACACCT 1223

Qy 301 LeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyr 320
Db 1224 TTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACTGGATTGTGGTCCCGGGGTAT 1283

Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
Db 1284 CACGCCCTTTACTGCCACGGAAGATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT 1343

Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360

Db 1344 AATCATGCCATTGTTACAGACGTTGGTCACTGTTAACTCTAAGATTCTTAAGCATGC 1403

Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
Db 1404 TGTGTCCCGCAGAACTCAGTGTCTATCTCGATGCTGTACCTTGACGAGAATGAAGGTT 1463

Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1464 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTCGC 1511

RESULT 14

US-09-804-625-3
; Sequence 3, Application US/09804625
; Publication No. US20030049826A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; Rosen, Vicki A.
; Wozney, John M.
; TITLE OF INVENTION: No. US20030049826A1el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/804,625
; FILING DATE: 09-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/925,779
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: 5160C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; CELL TYPE: Osteosarcoma Cell Line
; CELL LINE: U-2OS
; IMMEDIATE SOURCE:
; LIBRARY: U2OS cDNA in Lambda GT10
; CLONE: Lambda U2OS-39
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1546
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1202..1543
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 14..1607

FEATURE:

NAME/KEY: sig peptide
 LOCATION: 356-424
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-804-625-3

Alignment Scores:

Pred. No.: 9.43e-227 Length: 1607
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-801-648-2 (1-396) x US-09-804-625-3 (1-1607)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
 Db 356 ATGGTGGCGGAGCCCGCTGCTTCTAGCGTTGCTGTCCCGAGGTCCTCTCGGGCGGC 415
 Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgGlyPheAlaAlaAlaSerSerGlyArg 40
 Db 416 GCGGCTGGCCCTCGTTCCGAGCTGGCGCGCAGGAAGTTCCGCGCGCGCTCTCGGGCGGC 475
 Qy 41 ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 Db 476 CCTCATCCAGCCCTCTGACGAGGCTCTGAGCGAGTTCTGAGTTGCGGCTGCTCAGCATG 535
 Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu 80
 Db 536 TTCCGCTGAAACAGACAGACCCACCCAGCAGGAGCGCGTGGTGGTCCCGCTTACATGCTA 595
 Qy 81 AspleuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db 596 GACCTGTATCGAGGACATCTCAGGTGAGCGGGCTCACCCGCGCCAGACACCGGTTGAG 655
 Qy 101 ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu 120
 Db 656 AGGGCAGCAGCGGAGCCACACTGTGCGCAGCTTCCACCATGAAGATCTTTGGAAGA 715
 Qy 121 LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro 140
 Db 716 CTACAGAAACGAGTGGGAAACACACCGGAGATCTCTTTAAATTAAGTTCTATCCCC 775
 Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGluMetGlnAspAla 160
 Db 776 ACGGAGGAGTTTATCACCTCAGCAGAGCTTCAGGTTTCCGAGAACAGATGCAAGATGCT 835
 Qy 161 LeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleLeuLysProAla 180
 Db 836 TTAGGAACAATAGCAGTTTCCATCCGATATATATATATATATATATATATATATATAT 895
 Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 Db 896 ACAGCCAACTCGAAATTCCTCCGTGACAGACTTTTGGACACAGGTTGGTGAATCAGAAT 955
 Qy 201 AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly 220
 Db 956 GCAAGCGGTGGGAAAGTTTTCATGTCAACCCCGCTGTGATCGGTGCACTGCACAGGGA 1015
 Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
 Db 1016 CACGCCAACCATGGATTCGTGGTGGAGTGGCCACTTGGAGAGAGAACAGGTGTCTCC 1075
 Qy 241 LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 Db 1076 AAGAGACATGTTAGGATAGCAGGCTTTTGGACCAAGATGAACACAGCTGGTGCACAGATA 1135
 Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db 1136 AGGCCATTGCTAGTAACCTTTTGGCCATGATGGAAAGGGCATCTCTCCACAAAAGAGAA 1195
 Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300

Db 1196 AAACGTCAAGCCAAACACAAACAGCGGAAACGCCTTAAGTCAGCTGTGAAGACACCCCT 1255
 Qy 301 LeuTyrValAspPheSerAspValGlyTTPAsnAspTTPileValAlaProProGlyTyr 320
 Db 1256 TTGTACGTGGACTTCAGTGACGTGGGTGGAAATGACTGGATGTGGCTCCCGCGGGTAT 1315
 Qy 321 HisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db 1316 CACGCCTTTACTGCCACGGAGATGCCCTTTCTCTGGCTGATCATCTGAACCTCACT 1375
 Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCys 360
 Db 1376 AATCATGCCATTGTTGACAGCGTTGGTCAACTCTGTTAATCTTAAGATTCTTAAGCATGC 1435
 Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal 380
 Db 1436 TGTGTCCCGACAGAACTCAGTGCTATCTCGATCTGTACCTTGACGAGATGAAAGGTT 1495
 Qy 381 ValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
 Db 1496 GTATTAAAGAACTATCAGGACATGTTGTGGAGGTTGTGGGTGTGCG 1543

RESULT 15
 US-10-397-214-3
 ; Sequence 3, Application US/10397214
 ; Publication No. US20040009916A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Elizabeth A.
 ; APPLICANT: Rosen, Vicki A.
 ; APPLICANT: Wozney, John M.
 ; TITLE OF INVENTION: NO. US20040009916A1el BMP Products
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
 ; STREET: 87 CAMBRIDGE PARK DRIVE
 ; CITY: CAMBRIDGE
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/10/397,214
 ; FILING DATE: 27-MARCH-2003
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/721,847A
 ; FILING DATE: 14-JUN-1991
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kapinos, Ellen J.
 ; REGISTRATION NUMBER: 32,245
 ; REFERENCE/DOCKET NUMBER: 5160C
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-876-1170
 ; TELEFAX: 617-876-5851
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1607 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORGANISM: Homo Sapiens
 ; CELL TYPE: Osteosarcoma Cell Line
 ; CELL LINE: U-2OS

IMMEDIATE SOURCE:
 LIBRARY: U2OS cDNA in Lambda GT10
 CLONE: Lambda U2OS-39
 POSITION IN GENOME:

UNITS: bp

FEATURE:

NAME/KEY: CDS

LOCATION: 356..1546

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 1202..1543

FEATURE:

NAME/KEY: mRNA

LOCATION: 14..1607

FEATURE:

NAME/KEY: sig_peptide

LOCATION: 356..424

US-10-397-214-3

Alignment Scores:

Pred. No.: 9.43e-227 Length: 1607
 Score: 2098.00 Matches: 396
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-801-648-2 (1-396) x US-10-397-214-3 (1-1607)

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Db	416	GCGGCTGGCCCTGTTCCGGAGCTGGCGCGCAGGAAGTTCCGCGCGCGCTGCTCGCGCGC	475
Qy	41	ProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet	60
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Qy	61	PheGlyLeuLysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeu	80
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Qy	101	ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu	120
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Qy	121	LeuProGluThrSerGlyLysThrThrArgArgPhePhePheAsnLeuSerSerIlePro	140
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Qy	301	LeuTyrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyr	320
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Qy	321	HisAlaPheTyrCysHisGlyGluCysPheProPheProLeuAlaAspHisLeuAsnSerThr	340
Db	1316	CAGCCCTTTTACTGCCACGAGAAATGCCCTTTCTCTGGCTGATCATCTGAACCTCCACT	1375
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Qy	361	CysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysVal	380
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 Job time : 721 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2006, 23:57:41 ; Search time 207 Seconds
(without alignments)
1394.733 Million cell updates/sec

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Perfect score: 2098
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
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Database : Published Applications NA New.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2092	99.7	1260	7	US-11-051-568-4 Sequence 4, Appl
3	1927.5	91.9	2738	7	US-11-136-527-2371 Sequence 2371, Ap
4	1269	60.5	1751	6	US-10-650-326B-11 Sequence 11, Appl
5	1269	60.5	1788	7	US-11-051-568-6 Sequence 6, Appl
6	1255	59.8	1900	7	US-11-136-527-2142 Sequence 2142, Ap
7	1179	56.2	1586	7	US-11-051-568-18 Sequence 18, Appl
8	561.5	26.8	525	7	US-11-051-568-16 Sequence 16, Appl

9	554.5	26.4	1505	7	US-11-051-568-12 Sequence 12, Appl
10	546	26.0	1277	7	US-11-051-568-14 Sequence 14, Appl
11	544.5	26.0	1822	6	US-10-816-768-38 Sequence 38, Appl
12	544.5	26.0	1822	6	US-10-650-326B-17 Sequence 17, Appl
13	544.5	26.0	1822	7	US-11-051-568-1 Sequence 1, Appl
14	544.5	26.0	1878	7	US-11-186-284-9 Sequence 9, Appl
15	542	25.8	1873	6	US-10-650-326B-18 Sequence 18, Appl
16	542	25.8	1873	7	US-11-051-568-24 Sequence 24, Appl
17	534	25.5	2943	7	US-11-000-688-1535 Sequence 1535, Ap
18	534	25.5	5801	7	US-11-000-463-580 Sequence 580, App
19	525.5	25.0	600	7	US-11-136-527-6238 Sequence 6238, Ap
20	489.5	23.3	1926	6	US-10-650-326B-22 Sequence 22, Appl
21	489.5	23.3	1926	7	US-11-051-568-26 Sequence 26, Appl
22	487	23.2	1723	6	US-10-650-326B-20 Sequence 20, Appl
23	483	23.0	1723	7	US-11-051-568-28 Sequence 28, Appl
24	466	22.2	1459	7	US-11-136-527-607 Sequence 607, App
25	456.5	21.8	1004	7	US-11-051-568-10 Sequence 10, Appl
26	456	21.7	1400	7	US-11-136-527-4703 Sequence 4703, Ap
27	443.5	21.1	2703	7	US-11-191-072-1 Sequence 1, Appl
28	423	20.2	1252	6	US-10-131-826A-341 Sequence 341, App
29	421	20.1	3197	7	US-11-000-463-538 Sequence 538, App
30	421	20.1	3283	7	US-11-000-463-66 Sequence 66, Appl
31	418	19.9	1212	9	US-11-091-334-1 Sequence 1, Appl
32	397	18.9	314	7	US-11-051-568-33 Sequence 33, Appl
33	395	18.8	405	6	US-10-816-768-90 Sequence 90, Appl
34	385	18.4	1764	7	US-11-136-527-3392 Sequence 3392, Ap
35	383.5	18.3	2158	7	US-11-136-527-3797 Sequence 3797, Ap
36	375.5	17.9	516	7	US-11-051-568-8 Sequence 8, Appl
37	370.5	17.7	1840	7	US-11-186-284-88 Sequence 88, Appl
38	370.5	17.7	2017	6	US-10-821-234-107 Sequence 107, App
39	361.5	17.2	1419	7	US-11-092-353-7 Sequence 7, Appl
40	357.5	17.0	647	6	US-10-816-768-99 Sequence 99, Appl
41	336	16.0	1437	7	US-11-092-353-8 Sequence 8, Appl
42	329	15.7	745	7	US-11-136-527-1322 Sequence 1322, Ap
43	327.5	15.6	600	7	US-11-136-527-5418 Sequence 5418, Ap
44	326.5	15.6	2429	7	US-11-136-527-2792 Sequence 2792, Ap
45	326	15.5	1400	7	US-11-136-527-6467 Sequence 6467, Ap

ALIGNMENTS

RESULT 1
US-10-650-326B-10
; Sequence 10, Application US/10650326B
; Publication No. US20050272649A1
; GENERAL INFORMATION:
; APPLICANT: Hruska, Keith A.
; APPLICANT: McCartney, John B.
; APPLICANT: Charette, Marc F.
; TITLE OF INVENTION: CONJOINT ADMINISTRATION OF MORPHOGENS AND ACE INHIBITORS IN
; FILE REFERENCE: JJJ-P01-599
; CURRENT APPLICATION NUMBER: US/10/650,326B
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,431
; FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-650-326B-10

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Db 384 GCGGCTGGCCCTCGTTCCGGAGTCGGCCGACGAGGTTCCGGCGGCGGTCTGGGCGGC 443
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Db 624 AGGCGAGCCAGCCGAGCAACACTGTGCGCAGCTTCCACCATGAAGATCTTTGGAAGA 683
Qy 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
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; Sequence 4, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; OZKAYNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051.568
; FILING DATE: 04-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/321,799
; FILING DATE: 17-DEC-2002
; APPLICATION NUMBER: US 09/148,925
; FILING DATE: 8-SEP-1998
; APPLICATION NUMBER: US 08/449,699
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 1-NOV-1993
; APPLICATION NUMBER: US 07/841,646
; FILING DATE: 21-FEB-1992
; APPLICATION NUMBER: US 07/827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: US 07/579,865
; FILING DATE: 7-SEP-1990
; APPLICATION NUMBER: US 07/621,849
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/621,988
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/810,560
; FILING DATE: 20-DEC-1991
; APPLICATION NUMBER: US 07/569,920
; FILING DATE: 20-AUG-1990
; APPLICATION NUMBER: US 07/600,024
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; APPLICATION NUMBER: US 07/599,543
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/616,374
; FILING DATE: 21-NOV-1990
; APPLICATION NUMBER: US 07/483,913
; FILING DATE: 22-FEB-1990
; APPLICATION NUMBER: US 07/179,406
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: US 07/232,630
; FILING DATE: 15-AUG-1988
; APPLICATION NUMBER: US 07/315,342
; FILING DATE: 23-FEB-1989
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 FILING DATE: 17-OCT-1989
 APPLICATION NUMBER: US 07/422,613
 FILING DATE: 17-OCT-1989
 APPLICATION NUMBER: US 07/422,623
 FILING DATE: 17-OCT-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: DIANA M. STEEL
 REGISTRATION NUMBER: 43,153
 REFERENCE/DOCKET NUMBER: STR-001CP6C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/248-7000
 TELEFAX: 617/248-7100
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
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 HYPOTHETICAL: NO
 ANTI-SENSE: NO
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 ORGANISM: HOMO SAPIENS
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US-10-801-648-2 (1-396) x US-11-051-568-4 (1-1260)

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Db	69	CGCGCTGGCTCGTTCCGAGCTGGCGCGCAGGAAAGTTGGCGCGCGCGTGGCGCGC	128
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Db	129	CCCTCATCCACCCCTCTGACGAGGTCTGACGAGGTTCGAGTTGCGGCTGCTGACATG	188
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Db	729	AAGAGACATGTTAGGATAGCAGGTCTTTGACCAAGATGAACACAGCTGTGTACAGATA	788
Qy	261	ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu	280
Db	789	AGGCCATTTGCTAGTAACCTTTTGGCCATGATGGAAGAGGCGCATCTCTCCACAAAGAGA	848
Qy	281	LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro	300
Db	849	AAACGTCAAGCAACCAACCAACACGCGGAAACCGCTTAAGTCCAGCTGTGAAGAGACACCT	908
Qy	301	LeuThrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTrp	320
Db	909	TTGTACGTGGACTTCAGTGACGTGGGTGGAAATGATGATGATGATGATGATGATGATG	968
Qy	321	HisAlaPheTrpCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr	340
Db	969	CACGCCCTTTTACTGCCAGGAGATGCCCTTTCTCTGCTGCTGATCATCTGAACCTCACT	1028
Qy	341	AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysLysIleProLysAlaCys	360
Db	1029	AATCATGCCATTTGTTCCAGACGTTGTCACCTCTGTTAACTCTTAAGATTTCTTAAGGCA	1088
Qy	361	CysValProThrGluLeuSerAlaIleSerMetLeuThrLeuAspGluAsnGluLysVal	380
Db	1089	TGTGTCCCGACAGAACTCAGTGCTATCTCGATGCTGATGCTGATGCTGATGCTGATGCT	1148
Qy	381	ValLeuLysAsnTrpGlnAspMetValValGluGlyCysGlyCysArg	396
Db	1149	GTATTAAGAACTATCAGATATGTTTGTGGAGGGTGTGGGTGTGGTGTGGTGTGGTGT	1196

RESULT 3
 US-11-136-527-2371
 ; Sequence 2371, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2371
 ; LENGTH: 2738
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-11-136-527-2371

Alignment Scores:

Pred. No.: 7.03e-183 Length: 2738
 Score: 1927.50 Matches: 361
 Percent Similarity: 95.71% Conservative: 18
 Best Local Similarity: 91.16% Mismatches: 14
 Query Match: 91.87% Indels: 3
 DB: 7 Gaps: 2

US-10-801-648-2 (1-396) x US-11-136-527-2371 (1-2738)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
 Db ATGGTGGCGGAGACCCGCTGCTTCTAGTGTGCTTCTCCAGGCTCTCTCTGGCGGC 407
 Qy 21 AlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLaserSerGlyArg 40
 Db CGCGCCGCGCTCAATTCGGAGCTGGCGCGCAAGAAAGTTCCGCGGCGCATCSGCG- 461
 Qy 41 ProSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMet 60
 Db CCTATTCGCGGCTTCGAGAGAGTCTCTACGAGATTGAGTTGAGGCTGCTCAGCATG 521
 Qy 61 PheGlyLeuLysGlnArgProThrProSerArgAspAlaValProProTyrrMetLeu 80
 Db TTTGGCTTGAAGCAGAGACCCACCCCGCAGCAGCGTGGTGGTGGCCCTATATGCTC 581
 Qy 81 AspLeuTyrrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGlu 100
 Db GACCTGTACCGCGGCACTCGGGCAGCAGAGCGCTCGCCCGCAGACCCAGCGCTGGAG 641
 Qy 101 ArgAlaLaserArgAlaAenThrValArgSerPheHisGluGluSerLeuGluGlu 120
 Db AGGCGAGCGCCGCCCAACACCGTCTAGCTTCCATCAGGAAGAGCCATCGAGGAA 701
 Qy 121 LeuProGluThrSerGlyLysThrArgArgPhePheAsnLeuSerSerIlePro 140
 Db CTTTCAGAAATGAGTGGGAAAACITCCCGACGCTTCTTCTCAATTTAAGTTCTGTCCCT 761
 Qy 141 ThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAla 160
 Db ACTGATGAGTTTCTCACATCTGCAGAGCTCCAGATTTTTCGGGAACAAATGCAGGAAGCT 821
 Qy 161 LeuGlyAsnAsnSerSerPheHisArgLysLeuIleValLeuIleLysProAla 180
 Db TTGGGA--AATAGTAGTTTCCAGCACCGAATTAATATTATGAAATTTAAAGCCCTGCC 878
 Qy 181 ThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsn 200
 Db ACAGCCAGCTCAAAATTTCTGTGACCCAGACTATTGGACACCCAGGTTAGTGACTCAGAAC 938
 Qy 201 AlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGly 220
 Db ACAAGTCAGTGGGAGAGCTTTGATGTCCCGGCTGTGATCGATGCAGCAGCAGGGA 998
 Qy 221 HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer 240
 Db CACACCAACCATGGTTTGTGGTGAAGTGGCCCACTTAGAGGAGAAGCCAGGTGTCTCC 1058
 Qy 241 LysArgHisValArgLysSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIle 260
 Db AAGAGACATGTGAGATTAGCAGTCTTTGACCAAGATGACACACAGCTGGTCTCAGGTA 1118
 Qy 261 ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu 280
 Db AGACCACTGTGTAGTACTTTTGGCCAGCAGCGTAAAGGACATCCACTCCACAAACGAGAA 1178
 Qy 281 LysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisPro 300
 Db AAGCGTCAAGCCAAACAAACACGGAAGCGTCTTAAGTCCAGCTGCATCAAAAGCACCT 1238
 Qy 301 LeuTyrrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrr 320
 Db TTGTATGTGACTTTCATGTATGTGGGTGGNAAGACTGGATCGTGGGCCCTTCCAGGCTAT 1298

Qy 321 HisAlaPheTyrrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThr 340
 Db CATGCCCTTTTACTGCCCATGGGAATGCTCTTTCCCTGGCTGATCACTCACTCCACCC 1358
 Qy 341 AsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysLysIleProLysAlaCys 360
 Db AACCATGCCATAGTGCAGACTCTGGTAAACTCTGTGAATTCCAAATCCCTAAGGCATGC 1418
 Qy 361 CysValProThrGluLeuSerAlaIleSerMetLeuTyrrLeuAspGluAsnGluLysVal 380
 Db TGTGTCCCACTGAGCTTAGCGCAATCTCCATGTTGTACCTAGATGAAACGAAAGGTT 1478
 Qy 381 ValLeuLysAsnTyrrGlnAspMetValValGluGlyCysGlyCysArg 396
 Db GTGCTAAAAAACTATCAGGACATGTTGTGGAGGTTTGGCGGTGTGCGC 1526

RESULT 4

US-10-650-326B-11

; Sequence 11, Application US/10650326B
 ; Publication No. US20050272649A1

; GENERAL INFORMATION:

; APPLICANT: Hruska, Keith A.

; APPLICANT: McCartney, John E.

; APPLICANT: Charette, Marc P.

; TITLE OF INVENTION: CONJOINT ADMINISTRATION OF MORPHOGENS AND ACE INHIBITORS IN

; FILE OF INVENTION: TREATMENT OF CHRONIC RENAL FAILURE

; FILE REFERENCE: JJJ-P01-599

; CURRENT APPLICATION NUMBER: US/10/650,326B

; CURRENT FILING DATE: 2003-08-28

; PRIOR APPLICATION NUMBER: 60/406,431

; PRIOR FILING DATE: 2002-08-28

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11

; LENGTH: 1751

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-650-326B-11

Alignment Scores:

Pred. No.: 5.13e-117 Length: 1751
 Score: 1269.00 Matches: 258
 Percent Similarity: 73.19% Conservative: 45
 Best Local Similarity: 62.32% Mismatches: 87
 Query Match: 60.49% Indels: 24
 DB: 6 Gaps: 10

US-10-801-648-2 (1-396) x US-10-650-326B-11 (1-1751)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGly 20
 Db ATGATTCCTGTAACCAAGATGCTGATGCTGTTTATTATGCCAAGTCTCTGCTAGGAGGC 454
 Qy 21 Ala-----AlaGlyLeuValProGluLeuGlyArgArgLysPheAla-----Ala 35
 Db GCAGAGCCATGCTAGTTTGTATACCTGAGACGGGGAAGAAAAGTCGCGAGATTCAGGGC 514
 Qy 36 AlaSerGlyValArgProSerSerGlnProSerAspGluValLeuSerGluPheGluLeu 55
 Db CACGGGGAGGACCGCTCAGGGCAG---AGCATGAGCTCTCTGGGAGCTTCGAGGCG 571
 Qy 56 ArgLeuLeuSerMetPheGlyLeuLysGlnArgProThrProSerArgAspAlaValVal 75
 Db ACACCTTCTGCAGATGTTTGGGCTGCGCGCGCCCGCAGCTTAGCAAGAGTGCCTCAT 631
 Qy 76 ProProTyrrMetLeuAspLeuTyrrArgArgHisSerGlyGln----- 89
 Db CGCGACTTACATGCGGGATCTTTTACCGGCTTTCAGTCTGGGAGGAGGAGGAGAGCATC 691
 Qy 90 -----ProGlySerProAlaProAspHisArgLeuGluArgAlaLaserArgAlaAsn 107
 Db CACAGCAGCTGTTCTTGAATATCTT-----GAGCGCCGCGCCAGCCCGGCGCAC 739

108 ThrValArgSerPheHisGluGluSerLeuGluGluLeuProGluThrSerGlyLys 127
Db ACCGTGAGAGCTTCCACACGAGACATCTGGAGACATCCCGAGGACCATGTAAC 799
128 ThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGluPheIleThrSer 147
Db TCTGCTTTCTGCTTCTTAACTCAGCAGCATCCCTGAGAACGAGGTGATCTCCTCT 859
148 AlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPhe 167
Db GCAGAGCTTCGGCTCTCCGGGAGCAGGTGACACGAGGCGCTGATGGGAAGGGGCTTC 919
168 HisHisArgIleAsnIleTyrGluIleIleLys---ProAlaThrAlaAsnSerLysPhe 186
Db ---CACCGTATTAACATTATGAGTTATGAGCCCGCCGACGAGAGTGGTCCCTGGGCAC 976
187 ProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTyrGluSer 206
Db CTCATCACAGACTACTGACACGAGACTGGTCCACCAATGTGACACGGTGGGAACT 1036
207 PheAspValThrProAlaValMetArgTyrThrAlaGlnGlyHisAlaAsnHisGlyPhe 226
Db TTTGATGTGAGCCCTGCGCTCTTCCCTGGACCGGAGACGACCAAACTATGGGCTA 1096
227 ValValGluValAlaHisLeuGluGluLysGlnGlyValSerLysArgHisValArgIle 246
Db GCCATTGAGGTGATCCTCATCAGACTCGACCCACGAGGCGGACGATGTACGATT 1156
247 SerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuValThr 266
Db AGCGATCGTTACCTCAAGGAGTGGGAATTGGGCGGAGCTCCGCGCCCTCTCTGTACC 1216
267 PheGlyHisAspGlyLysGlyHisProLeu-----HisLysArgGluLysArgGlnAla 284
Db TTTTGCCCATGATGGCGGGGCGCATGCTTTCACCGACCGCGGAGGCGCAAGCGTAGCCCT 1276
285 Lys---HisLysGlnArgLysArgLysSer---SerCysLysArgHisProLeuTyr 302
Db AGCATCTACTCAGCGGCGGCGGAGAGAGATTAAGAACTCGCGGCGGCACTCGCTCTAT 1336
303 ValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisAla 322
Db GTGACTTCAGGATGTGGCTGGAATGACTGATTTGTGGTGGCCACAGGCTACCGGCC 1396
323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis 342
Db TTCTACTGCCATGGGAGCTGCCCTTTCCACTGCTGACCACTCAACTCAACCAACCAT 1456
343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362
Db GCCATTGTGCAGACCTGGTCAATTCTGTCAATTCAGTATCCCAAGGCGTGTGTGTG 1516
363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValValLeu 382
Db CCCACTGAGTGAAGTGCATCTCCATGCTGTACTGATGATGATGATGATGATGATGATG 1576
383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db AAAAATTATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1618

RESULT 5

US-11-051-568-6
; Sequence 6, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; OZKAYNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/051.568

FILING DATE: 04-Feb-2005

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 10/321,799

FILING DATE: 17-DEC-2002

APPLICATION NUMBER: US 09/148,925

FILING DATE: 8-SEP-1998

APPLICATION NUMBER: US 08/449,699

FILING DATE: 24-MAY-1995

APPLICATION NUMBER: US 08/147,023

FILING DATE: 1-NOV-1993

APPLICATION NUMBER: US 07/841,646

FILING DATE: 21-FEB-1992

APPLICATION NUMBER: US 07/827,052

FILING DATE: 28-JAN-1992

APPLICATION NUMBER: US 07/579,865

FILING DATE: 7-SEP-1990

APPLICATION NUMBER: US 07/621,849

FILING DATE: 4-DEC-1990

APPLICATION NUMBER: US 07/621,988

FILING DATE: 4-DEC-1990

APPLICATION NUMBER: US 07/810,560

FILING DATE: 20-DEC-1991

APPLICATION NUMBER: US 07/569,920

FILING DATE: 20-AUG-1990

APPLICATION NUMBER: US 07/600,024

FILING DATE: 18-OCT-1990

APPLICATION NUMBER: US 07/599,543

FILING DATE: 18-OCT-1990

APPLICATION NUMBER: US 07/616,374

FILING DATE: 21-NOV-1990

APPLICATION NUMBER: US 07/483,913

FILING DATE: 22-FEB-1990

APPLICATION NUMBER: US 07/179,406

FILING DATE: 08-APR-1988

APPLICATION NUMBER: US 07/232,630

FILING DATE: 15-AUG-1988

APPLICATION NUMBER: US 07/315,342

FILING DATE: 23-FEB-1989

APPLICATION NUMBER: US 07/660,162

FILING DATE: 22-FEB-1991

APPLICATION NUMBER: US 07/422,699

FILING DATE: 17-OCT-1989

APPLICATION NUMBER: US 07/422,613

FILING DATE: 17-OCT-1989

APPLICATION NUMBER: US 07/422,623

FILING DATE: 17-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 1788 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

```

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: HIPPOCAMPUS
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 403..1626
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; /product= "CMP2B"
; /evidence= EXPERIMENTAL
; /note= "CMP2B (CNA)"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-11-051-568-6

Alignment Scores:
Pred. No.: 5.29e-117 Length: 1788
Score: 1269.00 Matches: 258
Percent Similarity: 73.19% Conservative: 45
Best Local Similarity: 62.32% Mismatches: 87
Query Match: 60.49% Indels: 24
DB: 7 Gaps: 10

US-10-801-648-2 (1-396) x US-11-051-568-6 (1-1788)

Qy 1 MetValAlaGlyThrArgCysLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 403 ATGATTCTGTGTACCAAGATGCTGATGCTGTTTATTATGCTCAAGTCTCTGCTAGGAGC 462

Qy 21 Ala-----AlaGlyLeuValProGluLeuGlyArgGlyPheAla-----Ala 35
Db 463 GCGAGCCATGCTAGTTTGATACCTGAGACGCGGGAAGAAAGTCGCGAGATTTCAGGGC 522

Qy 36 AlaSerSerGlyArgProSerSerGlnProSerAspGluValLeuSerGluPheGluLeu 55
Db 523 CACCGCGGAGACCGCCGCTCAGGGCAG---AGCCATGAGCTCTGCGGGATCTTCGAGGCG 579

Qy 56 ArgLeuLeuSerMetPheGlyLeuLysGlnArgProThrProSerArgAspAlaValVal 75
Db 580 ACATTCTGTCAGATGTTGGCTGCGCGCGCGCCGAGCTAGCAAGATGCGCTCAT 639

Qy 76 ProProTyrMetLeuAspLeuTyrArgArgHisSerGlyGln----- 89
Db 640 CCGGACTACATCGCGGATCTTTACCGGCTTCAGTCTGGGAGGAGGAGGAGAGCAGATC 699

Qy 90 -----ProGlySerProAlaProAspHisArgLeuGluArgAlaAlaSerArgAlaAsn 107
Db 700 CACAGCACTGCTCTTGAGTATCTCT-----GAGCGCCGCGCCAGCGCGGCGCAAC 747

Qy 108 ThrValArgSerPheHisHisGluGluSerLeuGluGluProGluThrSerGlyLys 127
Db 748 ACCGTGAGGAGCTCCACCACAGAGACATCTGGAGACATCCCGAGGACCATGTAAC 807

Qy 128 ThrThrArgArgPhePheAsnLeuSerSerLeuProThrGluGluPheIleThrSer 147
Db 808 TCTGCTTTCTCTCTCTTTAACTCCTCAGCAGCATCCCTGAGAACGAGTGTCTCTCT 867

Qy 148 AlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPhe 167
Db 868 GCAGAGCTTCGGCTCTCTCCGGGAGCAGGTGGACCACGAGGCGCTGATTTGGAAAGGGGCTTC 927

Qy 168 HisHisArgIleAsnIleTyrGluIleIleLys---ProAlaThrAlaAsnSerLysPhe 186
Db 928 ---CACGCTATAACATTATGAGGTATGAGCCCGCCAGCAGAGTGGTCTCTGGGCAC 984

Qy 187 ProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTyrPgluSer 206
Db 985 CTCATCACGACTACTGGACACGAGCTGGTCCACCAATGTGCACACGCGTGGGAAACT 1044

Qy 207 PheAspValThrProAlaValMetArgTyrThrAlaGlnGlyHisAlaAsnHisGlyPhe 226

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Db 1045 TTTGATGTGAGCCCTCGGTCCTTCGCTGGACCGGAGAGAGCCAAATATGGGCTA 1104
Qy 227 ValValGluValAlaHisLeuGluGluGlyValSerLysArgHisValArgIle 246
Db 1105 GCCATTGAGTGACTACCTCCATCAGACTCGGACCCACAGGGCCAGCATGTTCAGGATT 1164
Qy 247 SerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValThr 266
Db 1165 AGCGGATCGTTTACCTCAAGGAGTGGGAATTTGGGCCCGAGCTCCGGCCCTCTCGGTCA 1224
Qy 267 PheGlyHisAspGlyLysGlyHisProLeu-----HisLysArgGluLysArgGlnAla 284
Db 1225 TTGGCCATGATGCGCGGCGCATGCTTGACCGACCGCGAGGGCCAGCGTAGCCCT 1284
Qy 285 Lys---HisLysGlnArgLysArgLeuLysSer---SerCysLysArgHisProLeuTyr 302
Db 1285 AAGCATCACTCACAGCGGCGCAGGAAGAATAAGAACTGCCGGCGCCACTCGCTCTAT 1344
Qy 303 ValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProGlyTyrHisAla 322
Db 1345 GTGGACTTCAGCGATGTGGGCTGGAATGACTGGGATTTGGGCCCCACAGGCTACAGGCC 1404
Qy 323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis 342
Db 1405 TTCTACTGCCATGCGGACTGCCCCCTTCCACTGGCTGACCACTCAACTCAACCAACCAT 1464
Qy 343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362
Db 1465 GCCATTGTGCAGACCCCTGGTCAATTCTGTCATTTCCAGTATCCCAAGCCCTGTTGTG 1524
Qy 363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValValLeu 382
Db 1525 CCCACTGAACCTGAGTGCATCTCCATGCTGTACTGCTGATGATGATAGTGTGTACTG 1584
Qy 383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1585 AAAAATTATCAGGAGATGGTAGAGGATGTGGGTGCCGC 1626

RESULT 6
US-11-136-527-2142
; Sequence 2142, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2142
; LENGTH: 1900
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2142

Alignment Scores:
Pred. No.: 1.47e-115 Length: 1900
Score: 1255.00 Matches: 256
Percent Similarity: 72.46% Conservative: 44
Best Local Similarity: 61.84% Mismatches: 90
Query Match: 59.82% Indels: 24
DB: 7 Gaps: 10

US-10-801-648-2 (1-396) x US-11-136-527-2142 (1-1900)

Qy 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 401 ATGATTCTGTGTACCAAGATGCTGATGCTGTTTATTATGCTCAAGTCTCTGCTAGGAGC 460

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Qy 21 Ala-----AlaGlyLeuValProGluLeuGlyArgArgLysPheAla-----Ala 35
Db |||||
461 GGCAGAGTCTAGTTGATCTAGACCGGGGAGAAAAGTCCGCGAGTTCAGGGC 520
Qy 36 AlaSerSerGlyArgProSerSerGlnProSerAspGluValLeuSerGluPheGluLeu 55
Db |||||
521 CACGGGGAGGACCGCGCTCAGGGCAG--AGCCATGAGCTCTCGGGGACTTCGAGGCG 577
Qy 56 ArgLeuLeuSerMetPheGlyLeuLysGlnArgProThrProSerArgAspAlaValVal 75
Db |||||
578 ACATCTTCGAGATGTTGGGCTGGCGCGCTCCGAGCGCGAGCAAGAGCGCGTCTATC 637
Qy 76 ProProTyrMetLeuAspLeuTyrArgArgHisSerGlyGln----- 89
Db |||||
638 CCGGATTACATGAGGATCTTTACCGGCTCCAGTCTGGGAGGAGGAGGAGAGAGCAG 697
Qy 90 -----ProGlySerProAlaProAspHisArgLeuGluArgAlaAlaSerArgAla 106
Db AGCCAGGGAACCGGCTTGAGTACCCT-----GAGSGTCTCTGCCAGCAGAGCC 745
Qy 107 AsnThrValArgSerPheHisHisGluSerLeuGluGluLeuProGluThrSerGly 126
Db |||||
746 AACCTGTGAGGAGTTTCCATCACAAGAACATCTGGAGAACATCCCGAGGACCAAGTGAG 805
Qy 127 LysThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGluPheIleThr 146
Db |||||
806 AGCTCTGCTTTCTGTTCTCTTTAACTCAGCAGCATCCAGAGAAATGAGTGTATCTCC 865
Qy 147 SerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSer 166
Db |||||
866 TCTGAGAGCTCCGGCTATTTCCGGAGCAGGTGGACCGGCGCTGACTGGGACAGGGC 925
Qy 167 PheHisHisArgIleAsnIleTyrGluLeuLeuLys-----ProAlaThrAlaAsnSerLys 185
Db |||||
926 TTC---CACCGTATTAACATTTATGAGGTATGAAGCCCGCCAGCAGAAATGCTGCTGGA 982
Qy 186 PheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAsnSerArgTrpGlu 205
Db |||||
983 CACCTCATCACAGCTACTGACACACAGACTAGTCTCATATGTGACAGCGGTGGGAA 1042
Qy 206 SerPheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsnHisGly 225
Db |||||
1043 ACTTTCGATGTAGCCCTCGAGTCTCTGATGACCCCGGAGAAACCAACCACTATGCG 1102
Qy 226 PheValValGluValAlaHisLeuGluLysGlnGlyValSerLysArgHisValArg 245
Db |||||
1103 CTGGCCATTGAGTGACTCACCTCCACACAGACACGCGCCACCGAGGCGCAACATGTGAG 1162
Qy 246 IleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuValVal 265
Db |||||
1163 ATTACCCATGTTTACCTCAGGGAGTGAATGGGCCCACTCCGGCCCTCTCTGCTC 1222
Qy 266 ThrPheGlyHisAspGlyLysGlyHisProLeu---HisLysArgGluLysArgGlnAla 284
Db |||||
1223 AYTTCGCGCAGATGGCGGGTCTATCTTACCCCGCGGAGGCGGCAAGGTAGTCCC 1282
Qy 285 Lys---HisLysGlnArgLysArgLeuLysSer---SerCysLysArgHisProLeuTyr 302
Db |||||
1283 AAGCATCACCCRCAGCGCTCCAGGAAGAATAAGAACTGCGCTCGCCATTCGCTCTAC 1342
Qy 303 ValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisAla 322
Db |||||
1343 GTGGAATTCAGTGAGTGGGCTGGAAATGATGATGATGCGTGGCGCCWCCAGGCTTACCAGGCC 1402
Qy 323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis 342
Db |||||
1403 TTCTACTGCCAGGGGACTGTCCTTTCCACTGGGCGGCCACTCACTCACTCAACCACTAT 1462
Qy 343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362
Db |||||
1463 GCCATTGTGACACCTGGTCACTCCGTTAATTTCTAGCATCTCCTAAGGCGCTGCTGTC 1522

Qy 363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValValLeu 382
Db |||||
1523 CCCACCGAATGAGCGCATTTCCATGTTGATCTGGACGAGTAGCACACAGGTGGTGTG 1582
Qy 383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db |||||
1583 AAAAATATCAGGAGATGTTGGTGGAGGGTGGCGATGCCGC 1624

RESULT 7
US-11-051-568-18
; Sequence 18, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; OZKAYNAK, ERGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/11/051,568
; FILING DATE: 04-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 10/321,799
; FILING DATE: 17-DEC-2002
; APPLICATION NUMBER: US 09/148,925
; FILING DATE: 8-SEP-1998
; APPLICATION NUMBER: US 08/449,699
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 1-NOV-1993
; APPLICATION NUMBER: US 07/841,646
; FILING DATE: 21-FEB-1992
; APPLICATION NUMBER: US 07/827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: US 07/579,865
; FILING DATE: 7-SEP-1990
; APPLICATION NUMBER: US 07/621,849
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/621,988
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/810,560
; FILING DATE: 20-DEC-1991
; APPLICATION NUMBER: US 07/569,920
; FILING DATE: 20-AUG-1990
; APPLICATION NUMBER: US 07/600,024
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/599,543
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/616,374
; FILING DATE: 21-NOV-1990
; APPLICATION NUMBER: US 07/483,913
; FILING DATE: 22-FEB-1990
; APPLICATION NUMBER: US 07/179,406
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: US 07/232,630
; FILING DATE: 15-AUG-1988
; APPLICATION NUMBER: US 07/315,342
; FILING DATE: 23-FEB-1989

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; APPLICATION NUMBER: US 07/660,162
; FILING DATE: 22-FEB-1991
; APPLICATION NUMBER: US 07/422,699
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,613
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,623
; FILING DATE: 17-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: DIANA M. STEEL
; REGISTRATION NUMBER: 43,153
; REFERENCE/DOCKET NUMBER: STK-001CP6C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1586 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1257
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; /product= "CBMP2B-2"
; /note= "CBMP2B-2 - FUSION"
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-11-051-568-18

Alignment Scores:
Pred. No.: 4,88e-108 Length: 1586
Score: 1179.00 Matches: 233
Percent Similarity: 74.86% Conservative: 38
Best Local Similarity: 64.36% Mismatches: 73
Query Match: 56.20% Indels: 18
DB: 7 Gaps: 7

US-10-801-648-2 (1-396) x US-11-051-568-18 (1-1586)

Qy 48 GluValLeuSerGluPheGluLeuArgLeuSerMetPheGlyLeuLysGlnArgPro 67
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 187 GAGTCTCTCGGGAGCTTCGAGCGGACACTTCGAGATGTTTGGGCTGCGCGCGCGCG 246
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 68 ThrProSerArgAspAlaValProProTyrMetLeuAspLeuTyrArgArgHisSer 87
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 247 CAGCTAGCAGAGTGGCGTCACTTCGGGACTACATCGGGATCTTTACCGGCTTCAGTCT 306
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 88 GlyGln-----ProGlySerProAlaProAspHisArgLeu 99
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 307 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 354
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 100 GluArgAlaAlaSerArgAlaAsnThrValArgSerPheHisGluGluSerLeuGlu 119
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 355 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 414
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 120 GluLeuProGluThrSerGlyLysThrThrArgPhePheAsnLeuSerSerIle 139
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 415 AACATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 474
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 140 ProThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAsp 159
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 475 CCTGAGAACGAGGCGATCTCTCTCGAGAGCTTCGGCTTCGCGGAGCGAGGAGGAGGAG 534
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 160 AlaLeuGlyAsnAsnSerSerPheHisArgIleAsnIleTyrGluIleLys---- 178
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 535 GGCCCTGATCGGAAAGGGGGCTTC---CACGATATAACATTATGAGGTTATGAGGCC 591
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 179 ProAlaThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsn 198
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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Db 592 CCAGCAGAGTGGTGGCTGGGCGACCTCATCACAGCACTACTGGACAGAGACTGGTCCAC 651
Qy 199 GlnAsnAlaSerArgTyrGluSerPheAspValThrProAlaValMetArgTyrThrAla 218
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 652 CACAATGTGACAGCGTGGGAACTTTTGTGAGCCCTCGGCTCTTCGCTGGACCCGG 711
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 219 GlnGlyHisAlaAsnHisGlyPheValValGluValAlaHisLeuGluLysGlnGly 238
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 712 GAGNAGCAGCAGCAACTATGGCTAGCCATTGAGGTGACTCACCTCCATCAGACTCGGACC 771
Qy 239 ValSerLysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTyrSer 258
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 772 CACGAGGCGCCAGCATGTGAGGATTTAGCGATTCCTCAAGGGAGTGGGAATTGGGCC 831
Qy 259 GlnIleArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeu----- 276
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 832 CAGCTCGGCGCCCTCTCTGGTCACTTTGGCCATGATGGCGGGCCCATGCCCTTACCCGA 891
Qy 277 HisLysArgGluLysArgGlnAlaLys--HisLysGlnArgLysArgLeuLysSer--- 294
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 892 CGCGGAGGCGGCGAGCGTAGCCCTTACGATCATCTCAGCGGCGCCAGAGAGATTAAG 951
Qy 295 SerCysLysArgHisProLeuTyrValAspPheSerAspValGlyTyrAsnAspTyrIle 314
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 952 AACTGCGGCGCCACTCGCTCTATGTGACTTCAGCGATGTGGCTGGAATGACTGGATT 1011
Qy 315 ValAlaProGlyTyrHisAlaPheTyrCysHisGlyGluCysProPheProLeuAla 334
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1012 GTGGCCCGCACAGCTACCGAGCCCTTCTACTGCGCATGGGAGCTGCCCTTTCCACTGGCT 1071
Qy 335 AspHisLeuAsnSerThrAsnHisAlaIleValGlnThrLeuValAsnSerValAsnSer 354
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1072 GACCACCTCAACTCAACCAACCATGCCATTGTGCAGACCTTGGTCAATTCGTCAATTC 1131
Qy 355 LysIleProLysAlaCysValProThrGluLeuSerAlaIleSerMetLeuTyrLeu 374
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1132 AGTATCCCAAGCGCTGTGTGCGCCACTGAAGTGAAGTGCATCTCCATCTGTACTGT 1191
Qy 375 AspGluAsnGluLysValValLeuLysAsnTyrGlnAspMetValValGluGlyCysGly 394
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1192 GATGAGTATGATAAGGTGGTACTGAAATAATTCAGGAGATGGTAGTAGAGGATGTGGG 1251
Qy 395 CysArg 396
Db 1252 TGCGCG 1257

RESULT 8
US-11-051-568-16
; Sequence 16, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; OZKAYNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568
; FILING DATE: 04-Feb-2005

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
FILING DATE: 17-DEC-2002
APPLICATION NUMBER: US 09/148,925
FILING DATE: 8-SEP-1998
APPLICATION NUMBER: US 08/449,699
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: US 08/147,023
FILING DATE: 1-NOV-1993
APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/827,052
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: US 07/579,865
FILING DATE: 7-SEP-1990
APPLICATION NUMBER: US 07/621,849
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/621,988
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/810,560
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 07/569,920
FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 07/600,024
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/599,543
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/616,374
FILING DATE: 21-NOV-1990
APPLICATION NUMBER: US 07/483,913
FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
FILING DATE: 08-APR-1988
APPLICATION NUMBER: US 07/232,630
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 07/315,342
FILING DATE: 23-FEB-1989
APPLICATION NUMBER: US 07/660,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,613
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,623
FILING DATE: 17-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
FEATURE:
NAME/KEY: CDS
LOCATION: 1..516
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "CBMP2B-1"
/note= "CBMP2B-1 - FUSION"
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-051-568-16

Alignment Scores:
Pred. No.: 1.05e-46 Length: 525
Score: 561.50 Matches: 105

Percent Similarity: 82.84% Conservative: 6
Best Local Similarity: 78.36% Mismatches: 14
Query Match: 26.76% Indels: 9
DB: 7 Gaps: 2
US-10-801-648-2 (1-396) x US-11-051-568-16 (1-525)
Qy 264 LeuValThrPheGlyHisAspGlyHisProLeuHisArgGluLysArgGln 283
Db 139 ATCGTTACTCCCGGCTCTCGTTACGTTGCGGATCTTAAGCAT----- 180
Qy 284 AlaLysHisLysGlnArgLysArgLeuLysSer---SerCysLysArgHisProLeuTyr 302
Db 181 -----CACTCACAGCGCGCCAGGAAGAATAAGAACTCCGCGCCCACTCGCTCTAT 234
Qy 303 ValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisAla 322
Db 235 GTGGACTTCAGCGATGCGGCTGGATGACTGGATTGTGGCCCAACCAAGGCTACCAAGGCC 294
Qy 323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis 342
Db 295 TTCTACTGCCATGGGAATGCCCTTCCCGCTAGCGGATCACTTCAACAGCAACCAACCAC 354
Qy 343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362
Db 355 GCCGTGGTGCAGACCTCTGTAACCTCTCAACTCCAGATCCCTAAGGCTTGCTGCGTG 414
Qy 363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValValLeu 382
Db 415 CCCACCGAGCTGTCCGCCATCAGCATGCTGTACCTGGACGAGATGAGAGTGTGTGCTG 474
Qy 383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 475 AAGAACTACCAAGAGATGGTAGAGGGCTGCGGCTGCGGC 516
RESULT 9
US-11-051-568-12
; Sequence 12, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; OZKAYNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H. L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568
; FILING DATE: 04-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/321,799
; FILING DATE: 17-DEC-2002
; APPLICATION NUMBER: US 09/148,925
; FILING DATE: 8-SEP-1998
; APPLICATION NUMBER: US 08/449,699
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 1-NOV-1993
; APPLICATION NUMBER: US 07/841,646

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; FILING DATE: 21-FEB-1992
; APPLICATION NUMBER: US 07/827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: US 07/579,865
; FILING DATE: 7-SEP-1990
; APPLICATION NUMBER: US 07/621,849
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/621,988
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/810,560
; FILING DATE: 20-DEC-1991
; APPLICATION NUMBER: US 07/569,920
; FILING DATE: 20-AUG-1990
; APPLICATION NUMBER: US 07/600,024
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/599,543
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/616,374
; FILING DATE: 21-NOV-1990
; APPLICATION NUMBER: US 07/483,913
; FILING DATE: 22-FEB-1990
; APPLICATION NUMBER: US 07/179,406
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: US 07/232,630
; FILING DATE: 15-AUG-1988
; APPLICATION NUMBER: US 07/315,342
; FILING DATE: 23-FEB-1989
; APPLICATION NUMBER: US 07/660,162
; FILING DATE: 22-FEB-1991
; APPLICATION NUMBER: US 07/422,699
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,613
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,623
; FILING DATE: 17-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: DIANA M. STEEL
; REGISTRATION NUMBER: 43,153
; REFERENCE/DOCKET NUMBER: STK-001CP6C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1505 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1452
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; /product= "OPIC"
; /note= "OPIC - FUSION"
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-11-051-568-12

Alignment Scores:
Pred. No.: 2,42e-45 Length: 1505
Score: 554.50 Matches: 145
Percent Similarity: 45.27% Conservative: 61
Best Local Similarity: 31.87% Mismatches: 137
Query Match: 26.43% Indels: 112
DB: 7 Gaps: 14

US-10-801-648-2 (1-396) x US-11-051-568-12 (1-1505)

Qy 20 GlyAlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaLaserSerGly 39
Db 186 GGCGCGCACAGCTTCGTGGCGCTCTGGGCACCCCTGTTCTGCTGGCGCTCGGCCCTGGC 245

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Qy 40 ArgProSerSerGlnPro-SerAspGluValLeuSerGluPhe----- 53
Db 246 CGA-----CTTCAGCCTGGACACAGAGTGCACTCGAGCTTCATCCACCGCGCCTCCG 299
Qy 54 -----GluLeuArgLeuLeuSerMetPheGlyLeuLysGlnAr 66
Db 300 CAGCAGGAGCGGGGAGATGCAGCGGAGATCTCTCCATTTTGGGCTTGCCTCCACCG 359
Qy 66 gProThrPro-----SerArgAspAlaValValProProTyrMetLeuAspLeuTy 83
Db 360 CCGCGCGCGCACCTCCAGGCAAGCACTCGGCACCCATGTTTCATGCTGGACCTGTA 419
Qy 83 rArgArgHisSerGly-----GlnProGlySer----- 92
Db 420 CAACGCCATCGCGGTGGAGGAGGGCGCGCGCGCGCGCGCTTCTCTACCCCTA 479
Qy 93 -----ProAlaProAspHisArgLeuGluArgAlaAl 103
Db 480 CAAGGCGCTTTCAGTACCCAGGCGCCCTCTGGCCAGCCTGCAGATGCCATTTCCT 539
Qy 103 aserArgAlaAsnThrValArgSerPhe----- 112
Db 540 CACCGAGCGGACATGCTCATGAGCTTCGTCGAACATCAACAAGGAATTCTT 599
Qy 113 -----HisHisGluGluSerLeuGluGluLeuProGluThrSerGlyLysTh 128
Db 600 CCACCCACGCTACCCCAT----- 618
Qy 128 rThrArgArgPhePhePheAsnLeuSerSerIleProThrCluGluPheIleThrSerAl 148
Db 619 -----CGAGAGTTCGGTTTATCTTCCAGATCCCAAGAGGGGAAGCTGTCAGGAGC 674
Qy 148 aGluLeuGlnValPheArgGluMetGlnAspAlaLeuGlyAsnAsnSerSerPheHi 168
Db 675 CGAATTCGGGATCTACAAGGACTACATCCGGGAACGTTCCAGCATGAGACG----- 726
Qy 168 sHisArgIleAsnIleTyrGluIleLeuLysPro-----AlaThrAlaAsnSerLysPh 186
Db 727 -TTCCGGATCAGCGTTTATCAGGTGCTCCAGGAGCACTTGGCGCAGGGAATCGATCTCT 785
Qy 186 eProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTTPGluse 206
Db 786 C-----CTGCTCGACGCGTACCTCTGGCGCTCGAGAGGCGCTGGCTGGT 833
Qy 206 rPheAspValThrProAlaValMetArgTTPThrAlaGlnGlyHisAlaAsnHisGlyPh 226
Db 834 GTTGACATCACAGCCACCAACCACTGGTGGTCAATCCGCGGCAACCTGGGCGCT 893
Qy 226 eValValGluValAlaHisLeuGluGluLysGlnGlyValSerLysArgHisValArgIl 246
Db 894 GCAGCTCTCGGTGGAGACGCTGGATGGGCAGATCAACCCCAAGTTGGCGGCGCTGAT 953
Qy 246 eSerArgSerLeuHisGlnAspGluHisSerTTPSerGlnIleArgProLeuLeuValTh 266
Db 954 TGGGCGG-----CACGGGCGCCAGAACAGCAGCGCTTCATGGTGGC 995
Qy 266 rPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGluLysArgGlnAlaLysHi 286
Db 996 TTTC-----TTCAAGGCCACGGAGGTCCACTTCGCGAGCATCCGGTCCACGGGGAG 1046
Qy 286 sLysGlnArgLysArgLeuLysSer----- 294
Db 1047 CAACAGCGCAGCAGAACCGCTCCAGAGACGCCCAAGAACCCAGGAAGCCCTTCGCGATGGC 1106
Qy 295 -----SerCysLysArgHisProLeuTy 302
Db 1107 CAACGTGGCAGAGAACAGCAGCAGCGGACCGAGAGCGGCTGTAAAGACGACGAGCTGTA 1166
Qy 302 rValAspPheSerAspValGlyTTPAsnAspTTPIleValAlaProGlyTyrHisAl 322
Db 1167 TGTCAAGTTCGAGACCTGGGCTGGCAGGAGTGGATCATCGCGCTGAGAGCTACGCGC 1226

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QY 322 aPheTyrcysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHi 342
Db 1227 CTACTACTGTGAGGGGAGTGTGCTTCCCTCTGAACCTCTACATGACGCCACCA 1286
QY 342 sAlaIleValGlnThrLeuValAsnSerValAsnSerLys---IleProLysAlaCysCy 361
Db 1287 CCCCATCGTCGACGCTGTCCACTTCATCAACCGGAACGGTGCACAGCCCTGTG 1346
QY 361 sValProThrGluLeuSerAlaIleSerMetLeuTyrlLeuAspGluAsnGluLysValVa 381
Db 1347 TCGGCCACGACGCTCAATGCCATTCCTCGCTCTACTTCGATGACAGTCCACGTCAT 1406
QY 381 lleuLysAsnTyrlGlnAspMetValValGluGlyCysGlyCys 395
Db 1407 CCTGAAGAAATACAGAAACATGTGTGTCGGGCTGTGGCTGC 1449

RESULT 10

US-11-051-568-14
; Sequence 14, Application US/11051568
; Publication No: US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; OZKAYNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568
; FILING DATE: 04-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/321,799
; FILING DATE: 17-DEC-2002
; APPLICATION NUMBER: US 09/148,925
; FILING DATE: 8-SEP-1998
; APPLICATION NUMBER: US 08/449,699
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 1-NOV-1993
; APPLICATION NUMBER: US 07/841,646
; FILING DATE: 21-FEB-1992
; APPLICATION NUMBER: US 07/827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: US 07/579,865
; FILING DATE: 7-SEP-1990
; APPLICATION NUMBER: US 07/621,849
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/621,988
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/810,560
; FILING DATE: 20-DEC-1991
; APPLICATION NUMBER: US 07/569,920
; FILING DATE: 20-AUG-1990
; APPLICATION NUMBER: US 07/600,024
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/599,543
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/616,374
; FILING DATE: 21-NOV-1990

; APPLICATION NUMBER: US 07/483,913
; FILING DATE: 22-FEB-1990
; APPLICATION NUMBER: US 07/179,406
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: US 07/232,630
; FILING DATE: 15-AUG-1988
; APPLICATION NUMBER: US 07/315,342
; FILING DATE: 23-FEB-1989
; APPLICATION NUMBER: US 07/660,162
; FILING DATE: 22-FEB-1991
; APPLICATION NUMBER: US 07/422,699
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,613
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,623
; FILING DATE: 17-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: DIANA M. STEEL
; REGISTRATION NUMBER: 43,153
; REFERENCE/DOCKET NUMBER: STK-001CP6C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1224
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; /product= "Op1D"
; /note= "Op1D - FUSION"
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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Score: 546.00 Matches: 130
Percent Similarity: 46.45% Conservative: 60
Best Local Similarity: 31.78% Mismatches: 123
Query Match: 26.02% Indels: 96
DB: 7 Gaps: 12
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QY 52 GluPheGluLeuArgLeuLeuSerMetPheGlyLeuLysGlnArgProThrPro----- 69
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QY 70 ---SerArgAspAlaValProProTyrlMetLeuAspLeuTyrlArgArgHisSerGly 88
Db 148 CAGGCAAGACCAACTCGGACCCCATGTTCTGCTGACCTGTACAAACGCCATGCGGT 207
QY 89 -----GlnProGlySer----- 92
Db 208 GGAGGAGGCGCGCGCGCGCGGCTTCTCTACCCCTACAGCGCGCTTCTCACT 267
QY 93 -----ProAlaProAspHisArgLeuGluArgAlaAlaSerArgAlaAsnThr 108
Db 268 ACCCAGGCGCGCGCTCTGCGCAGCTGCAAGATAGCATTTTCTCACCGACGCGACATG 327
QY 109 ValArgSerPhe-----His 113
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QY 114 HisGluGluSerLeuGluLeuProGluThrSerGlyLysThrArgArgPhePhe 133

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Db 388 CAT-----CGAGATTCCGG 402
Qy 134 PheAenLeuSerSerIleProThrGluGluPheIleThrSerAlaGluLeuValPhe 153
Db 403 TTTGATCTTTCAGATCCAGAGGGGAGCTGTCCAGCGCAGCGCAATTCCGGATCTAC 462
Qy 154 ArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPheHisHisArgIleAsnIle 173
Db 463 AAGGACTATATCCCGGACGGTTTCGACATGAGACG-----TTCCGGATCAGCGTT 513
Qy 174 TyrGluIleIleLysPro-----AlaThrAlaAsnSerLysPheProValThrArgLeu 191
Db 514 TATCAGTGTCTCCAGGACCACTTGGCAGGGAATCCGATCTCTTC-----CTG 561
Qy 192 LeuAspThrArgLeuValAsnGlnAsnAlaSerArgTrpGluSerPheAspValThrPro 211
Db 562 CTCGACAGCCGTCACCTCTGGCCCTCGGAGGAGGCGTGGTGTGTGATCATCACAGCC 621
Qy 212 AlaValMetArgTrpThrAlaGlnGlyHisAlaAsnHisGlyPheValValGluValAla 231
Db 622 ACCAGCAACCACTGGGTGTCAATCCGCGGCACAACTTGGGCCCTGCAGCTCTCGGTGAG 681
Qy 232 HisLeuGluGlnLysGlnGlyValSerLysArgHisValArgIleSerArgSerLeuHis 251
Db 682 ACGTGTGATGGCAGAGCATCAACCCAGTTGGCGGCGCTGATTTGGCGG-----732
Qy 252 GlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValThrPheGlyHisAspGly 271
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Qy 272 LysGlyHisProLeuHisLysArgGluLysArgGlnAlaLysHisLysGlnArgLysArg 291
Db 775 AAGCCACCGGAGGTCCACTTCGCGAGCATCCGGTCCACGGGGAGCAACAGCGCAGCAG 834
Qy 292 LeuLysSer-----294
Db 835 AACGCTCCAGAGCGCCCAAGAACCCAGGAGCCCTCGGATGGCCACAGTGGCAGAGAAC 894
Qy 295 -----SerCysLysArgHisProLeuTrpValAspPheSerAsp 307
Db 895 AGCAGCAGCGCAGAGCAGCGCTGTAAAGAACAGCAGAGCTGTATGTTCAGCTTCCGAGAC 954
Qy 308 ValGlyTrpAsnAspTrpIleValAlaProProGlyTrpHisAlaPheTrpCysHisGly 327
Db 955 CTGGGTGGCAGGACTGTGATCATCGCGCTGAAGGCTACGCGCTACTACTGTGAGGGG 1014
Qy 328 GluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHisAlaIleValGlnThr 347
Db 1015 GAGTGTGCTTCCCTCTGAACCTCTACATGACGCCACCAACAGCCATCGTCGACAGC 1074
Qy 348 LeuValAsnSerValAsnSerLys---IleProLysAlaCysCysValProThrGluLeu 366
Db 1075 CTGGTCCACTTCATCAACCCGGAACGGTGCACAGCCCTGCTGTGCGCCACGACGCTC 1134
Qy 367 SerAlaIleSerMetLeuTrpLeuAspGlnAsnGlnLysValValLeuLysAsnTrpGln 386
Db 1135 AATGCCATCTCCGCTCTACTTCGATGACAGCTCCCAACGTCATCTCTGAAGAAATACAGA 1194
Qy 387 AspMetValValGluGlyCysGlyCys 395
Db 1195 AACATGTGTGTCGGGCTGTGGTGTG 1221
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RESULT 11

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US-10-816-768-38
; Sequence 38, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-075
; CURRENT APPLICATION NUMBER: US/10/816,768
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; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 38
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (49)..(1341)
; OTHER INFORMATION: Morphogenic Protein OP1
US-10-816-768-38
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Alignment Scores:

Pred. No.:	3,21e-44	Length:	1822
Score:	544.50	Matches:	147
Percent Similarity:	45.39%	Conservative:	60
Best Local Similarity:	32.24%	Mismatches:	136
Query Match:	25.95%	Indels:	114
DB:	6	Gaps:	14

US-10-801-648-2 (1-396) x US-10-816-768-38 (1-1822)

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Qy 20 GlyAlaAlaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGly 39
Db 75 GGGCCCGCACAGCTTCGTGGCGCTTCTGGGCACCCCTGTTCTCTGCTGCGCTCCGCCCTGGC 134
Qy 40 ArgProSerSerGlnPro-SerAspGluValLeuSerGluPhe-----53
Db 135 CGA-----CTTCAGCTTGGACAACAGAGTGCATCGAGCTTCATCCACCGGCGCTCCG 188
Qy 54 -----GluLeuArgLeuLeuSerMetPheGlyLeuLysGlnAr 66
Db 189 CAGCCAGGAGCGCGGAGATGCAGCGCGAGATCTCTCCATTTTGGGCTTGGCCACCG 248
Qy 66 qProThrPro-----SerArgAspAlaValProProTrpMetLeuAspLeuTy 83
Db 249 CCGCGCGCCGACCTCCAGGGCAAGCAAACTCGGCAACCATGTTTCATGCTGGACCTGTA 308
Qy 83 rArgArgHisSerGly-----88
Db 309 CAA-CGCCATGGCGTGGAGGAGCGCGCGCGCGCGCGCGCTTCTCTACCCCT 367
Qy 89 -----GlnProGlySerProAlaProAsp-----96
Db 368 ACAAGGCCGTCTTCAGTACCCAGCGGCCCTCTCTGGCCAGCTGCAAGATAGCATTTCC 427
Qy 97 -HisArg-LeuGluArgAlaAlaSerArgAlaAsnThrValArg-----110
Db 428 TCACCGACCGCGATCGTTCATGAGCTTCGTCAACCTCGTGGAAACATGACAGGAATTC 487
Qy 111 -----SerPheHisHisGluLeuSerLeuGluGluLeuProGluThrSerGlyLysT 128
Db 488 TCCACCCACGCTACCACAT-----507
Qy 128 hrThrArgArgPhePheAsnLeuSerSerIleProThrGluGluPheIleThrSerA 148
Db 508 -----CGAGAGTTCGGGTTTGATCTTTTCCAAGATCCCAAGAGGGAAGCTGTCCAGCGCAG 562
Qy 148 laGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPheH 168
Db 563 CCGAAATTCGGATCTCAAGGACTACATCCGGGAACGCTTCGACAGATGAGACG-----615
Qy 168 ishHisArgIleAsnIleTrpGluIleLysPro-----AlaThrAlaAsnSerLysP 186
Db 616 --TTCCGGATCAGCGTTTATCAGGTGCTCCAGGAGCACTTGGCGAGGAATCGGATCTCT 673
Qy 186 heProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTrpGln 206
Db 674 TC-----CTGCTCGACAGCGGTATCCCTCTGGCGCTCGGAGGAGCGGTGGTGG 721
Qy 206 erPheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsnHisGlyP 226
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Db 722 TGTTGACATCAACAGCCACCAACCACTGGGTGGTCAATCCGGGCACCAACCTGGGCC 781
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Qy 266 hrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlnLysArgGlnAlaLysH 286
Db 884 CTTTC-----TTCAAGGCCACGAGGTCCACTTCGGCAGCATCCGGTCCACGGGGA 934
Qy 286 leLysGlnArgLysArgLeuLysSer-----CACGGGCCCCAGAACCAAGCAGCCCTTCATGGTGG 883
Db 935 GCMAACAGCGCAGCAGAACCGCTCCAGACGCCCCCAAGAACCAAGCAGCCCTTCATGGTGG 994
Qy 295 -----SerCysLysArgHisProLeuT 302
Db 995 CCAACGTGGCAGAGAACAGCAGCAGCAGCAGCGCTGTAAAGAACAGCAGAGTGT 1054
Qy 302 yrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisA 322
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RESULT 12

US-10-650-326B-17
; Sequence 17, Application US/10650326B
; Publication No. US20050272649A1
; GENERAL INFORMATION:
; APPLICANT: Hruska, Keith A.
; APPLICANT: McCartney, John E.
; APPLICANT: Charette, Marc F.
; TITLE OF INVENTION: CONJOINT ADMINISTRATION OF MORPHOGENS AND ACE INHIBITORS IN
; TITLE OF INVENTION: TREATMENT OF CHRONIC RENAL FAILURE
; FILE REFERENCE: JJJ-P01-599
; CURRENT APPLICATION NUMBER: US/10/650,326B
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,431
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 1822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-650-326B-17

Alignment Scores:

Pred. No.:	3,21e-44	Length:	1822
Score:	544.50	Matches:	147
Percent Similarity:	45.3%	Conservative:	60
Best Local Similarity:	32.24%	Mismatches:	136
Query Match:	25.95%	Indels:	114
DB:	6	Gaps:	14

US-10-801-648-2 (1-396) x US-10-650-326B-17 (1-1822)
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Qy 83 rArgArgHisSerGly----- 88
Db 309 CAA-CGCCATGGCGGTGGAGGAGGCGCGCGCGCGCGCGCTTCTCTACCCCT 367
Qy 89 -----GlnProGlySerProAlaProAsp----- 96
Db 368 ACAAGGCCGTCTTCAGTACCCAGGCGCCCTCTCTGGCCAGCCTGCAGATAGCCATTTCC 427
Qy 97 -HisArg-LeuGluArgAlaAlaSerArgAlaAsnThrValArg----- 110
Db 428 TCACCGAGCGCAGCATGTCATGAGCTTCGTCAACCTCTGGAACTGACAGGAATCT 487
Qy 111 -----SerPheHisGlyGluSerLeuGluLeuProGluThrSerGlyLysT 128
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Db 935 GCMAACAGCGCAGCAGAACCGCTCCAGACGCCCCCAAGAACCAAGCAGCCCTTCGCGATGG 994
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RESULT 13
US-11-051-568-1
; Sequence 1, Application US/11051568
; Publication No. US20050255141A1
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; OZKATNAK, ENGIN
; KUBERASAMPATH, THANGAVEL
; RUEGER, DAVID C.
; PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/051,568
; FILING DATE: 04-Feb-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/321,799
; FILING DATE: 17-DEC-2002
; APPLICATION NUMBER: US 09/148,925
; FILING DATE: 8-SEP-1998
; APPLICATION NUMBER: US 08/449,699
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 1-NOV-1993
; APPLICATION NUMBER: US 07/841,646
; FILING DATE: 21-FEB-1992
; APPLICATION NUMBER: US 07/827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: US 07/579,865
; FILING DATE: 7-SEP-1990
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; APPLICATION NUMBER: US 07/621,988
; FILING DATE: 4-DEC-1990
; APPLICATION NUMBER: US 07/810,560
; FILING DATE: 20-DEC-1991
; APPLICATION NUMBER: US 07/569,920
; FILING DATE: 20-AUG-1990
; APPLICATION NUMBER: US 07/600,024
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; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/599,543
; FILING DATE: 18-OCT-1990
; APPLICATION NUMBER: US 07/616,374
; FILING DATE: 21-NOV-1990
; APPLICATION NUMBER: US 07/483,913
; FILING DATE: 22-FEB-1990
; APPLICATION NUMBER: US 07/179,406
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: US 07/232,630
; FILING DATE: 15-AUG-1988
; APPLICATION NUMBER: US 07/315,342
; FILING DATE: 23-FEB-1989
; APPLICATION NUMBER: US 07/660,162
; FILING DATE: 22-FEB-1991
; APPLICATION NUMBER: US 07/422,699
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,613
; FILING DATE: 17-OCT-1989
; APPLICATION NUMBER: US 07/422,623
; FILING DATE: 17-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: DIANA M. STEEL
; REGISTRATION NUMBER: 43,153
; REFERENCE/DOCKET NUMBER: STK-001CP6C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: HIPPOCAMPUS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; /product= "Opi"
; /evidence= EXPERIMENTAL
; /standard name= "Opi"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-11-051-568-1

Alignment Scores:
Pred. No.: 3,21e-44 Length: 1822
Score: 544.50 Matches: 147
Percent Similarity: 45.39% Conservative: 60
Best Local Similarity: 32.24% Mismatches: 136
Query Match: 25.95% Indels: 114
DB: 7 Gaps: 14

US-10-801-648-2 (1-396) x US-11-051-568-1 (1-1822)
Qy 20 GlyAlaalaGlyLeuValProGluLeuGlyArgArgLysPheAlaAlaAlaSerSerGly 39
Db 75 GCGCGCGACAGCTTCGTGGCGCTCTGGGACCCCTGTTCCTGCTGCGCTCCGCCCTGGC 134
Qy 40 ArgProSerSerGlnPro-SerAspGluValLeuSerGluPhe----- 53
Db 135 CGA-----CTTCAGCTTGGACACGAGGTGCATCGAGCTTCATCCACCGCGCGCTCCG 188
Qy 54 -----GluLeuArgLeuSerMetPheGlyLeuLysGlnAr 66
Db 189 CAGCCAGGAGCGCGGGAGATGCAGCGAGATCTCTCCATTTTGGGCTTGGCCACC 248
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Qy 66 gProthrPro-----SerArgAspAlaValProProTyrMetLeuAspLeuTy 83
Db 249 CCGCGCGCGCACCTCCAGGGCAAGCACAACTCGCACCCCATGTTTCAGCTGGACCTGTA 308
Qy 83 rArgArgHisSerGly----- 88
Db 309 CAA-CGCGCATGCGGTGGAGGAGGCGCGCGCGCGCGCGCGCGCTTCCTACCCCT 367
Qy 89 -----GlnProGlySerProAlaProsp----- 96
Db 368 ACAAGCGCGTTCAGTACCGAGGCGCCCTCTCGCCAGCGCTGCAAGATAGCCATTTCC 427
Qy 97 -HisArg-LeuGluAlaAlaSerArgAlaAsnThrValArg----- 110
Db 428 TCACCGAGCGCACATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487
Qy 111 -----SerPheHisGluGluSerLeuGluLeuProGluThrSerGlyLysT 128
Db 488 TCCACCCAGCTACCCACAT----- 507
Qy 128 hrThrArgArgPhePheAsnLeuSerSerIleProThrGluGluPheIleThrSerA 148
Db 508 -----CGAGAGTTCGGTGTGATCTTCCAGATCCCAAGAGGGGAAGCTGTACGGCAG 562
Qy 148 laGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPheH 168
Db 563 CCGAATTCGGATCTACAGGACTACATCCGGGACGCTTCACATCAGAGC----- 615
Qy 168 isHisArgIleAsnIleTyrGluIleIleLysPro-----AlaThrAlaAsnSerLysP 186
Db 616 --TTCGGATGATCGCTTATCAGGTGCTCCAGAGCAGCTTGGGAGGGAATCGGATCTCT 673
Qy 186 heProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTrpGluS 206
Db 674 TC-----CTGCTCGACAGCCGTACCTCTGGGCGCTCGGAGGAGGCTGGCTGG 721
Qy 206 erPheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsnHisGlyP 226
Db 722 TGTTCATCATCACCCACCCAGCACCACTGGGTGCTCATTCGCGGCGCACACCTGGGCGC 781
Qy 226 heValValGluValAlaHisLeuGluGluGlyValSerLysArgHisValArgI 246
Db 782 TGCAGCTCTCGGTGGAGAGCGCTGGATGGCAGAGCATCAACCCCAAGTTGGCGGCGCTGA 841
Qy 246 leSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValT 266
Db 842 TTGGCGCG-----CACGGCGCCCGAGAACAGCAGCGCTTCATGTGG 883
Qy 266 hrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGluLysArgGlnAlaLysH 286
Db 884 CTTTC-----TTCAGGCGCACGAGGTCCACTTCGCGAGCATCCGCTCCAGCGGGA 934
Qy 286 isLysGlnArgLysArgLeuLysSer----- 294
Db 935 GCAACAGCGCGACCGCAGAACCGCTCCAGACGCCCCAGAACCGCCCTGCGGATGG 994
Qy 295 -----SerCysLysArgHisProLeuT 302
Db 995 CCAAGCTGCGCAGAGAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTGT 1054
Qy 302 yrValAspPheSerAspValGlyTyrAsnAspTrpIleValAlaProProGlyTyrHisA 322
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Db 1115 CCTACTACTGTGAGGGGAGTGTGCTTCCTCTGAGCTCTGAGCTGAGCGCCACCAACC 1174
Qy 342 isAlaIleValGlnThrLeuValAsnSerValAsnSerLys-----IleProLysAlaCysC 361
Db 1175 AGCCATCGTCAGAGCGCTGTGTCCACTTCATCAACCGCGGAAAGCGTGCACAGCCCTGT 1234
Qy 361 yaValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValV 381

Db 1235 GTGCGCCACGACGCTCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGCTCA 1294
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; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (123)...(1418)
US-11-186-284-9
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Best Local Similarity: 32.24% Mismatches: 136
Query Match: 25.95% Indels: 114
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US-10-801-648-2 (1-396) x US-11-186-284-9 (1-1878)
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Db 149 GGCGCGCGCACAGCTTGTGGGCGCTCTGGGCGACCCCTGTCTCTGCTGCGCTCGCCCTGC 208
Qy 40 ArgProSerSerGlnPro-SerAspGluValLeuSerGluPhe----- 53
Db 209 CGA-----CTTCAGCTGGACAGAGGTGACCTCGAGCTTCATCCACCGCGCGCTCCG 262
Qy 54 -----GluLeuArgLeuLeuSerMetPheGlyLeuLysGlnAr 66
Db 263 CAGCAGGAGCGGGGAGATGACGCGGAGATCTCTCCATTTTGGGCTTGCCCCCACC 322
Qy 66 gProThrPro-----SerArgAspAlaValProProTyrMetLeuAspLeuTy 83
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Qy 83 rArgArgHisSerGly----- 88


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Qy 140 oThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAl 160
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Qy 160 aLeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrGluIleIleLysProAl 180
Db 652 ATTTGACAAACGAGACC-----TTCAGATCACAGTCTATCAGGTGCTCCAGGAGCA 702
Qy 180 aThrAlaAsnSerLys-----PheProValThrArgLeuLeuAspThrArgLeuValAs 198
Db 703 CTCAGGAGGGAGTCCGACCTTTC-----TTGCTGGACACCGCACCACTCTG 750
Qy 198 nGlnAsnAlaSerArgTTrpGluSerPheAspValThrProAlaValMetArgTTrpThrAl 218
Db 751 GGTCTCTGAGGAGGGCTGTTGGTGTGTGATATCACAGCCACCACTGGGTGGT 810
Qy 218 aGlnGlyHisAlaAsnHisGlyPheValValGluValAlaHisLeuGluLysGlnGl 238
Db 811 CAACCCCTCGGCACACACCTGGGCTTACAGCTCTCTGTGGAGACCCCTGGATGGGCAGAGCAT 870
Qy 238 yValSerLysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSe 258
Db 871 CAACCCCAAGTTGGCAGCGCTGATTGGACGG-----CATGGACCCCA 912
Qy 258 rGlnIleArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLy 278
Db 913 GAACAGCAACACCTTCATGTTGGCTTC-----TTCAAGGCCACCGAAGTCCATCT 963
Qy 278 sAtGluLysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSer----- 294
Db 964 CGGTAGTATCGGTCCACGGGGGCAAGCAGCGCAGCCAGCAATCGCTCCAAGACGCCAAA 1023
Qy 294 ----- 294
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Qy 295 -SerCysLysArgHisProLeuTyrValAspPheSerAspValGlyTTrpAsnAspTrpIl 314
Db 1084 GGCCTGCAAGAAACATGAGCTGTAGCTTCCAGACCTTGGCTGGCAGGACTGGAT 1143
Qy 314 eValAlaProGlyTyrHisAlaPheTyrCysHisGlyGluCysPropheProLeuAl 334
Db 1144 CATTGCACCTGAAGGCTATGCTGCTACTACTGTGAGGAGAGTGGCTTCCCTCTGAA 1203
Qy 334 aAspHisLeuAsnSerThrAsnHisAlaIleValGlnThrLeuValAsnSerValAsn-- 353
Db 1204 CTCCTACATGAACGCCACCAACACGCCATCGTCCAGACACTGGTTTCATCATCAACCC 1263
Qy 354 -SerLysIleProLysAlaCysCysValProThrGluLeuSerAlaIleSerMetLeuTy 373
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Qy 373 rLeuAspGluAsnGluLysValValLeuLysAsnTyrGlnAspMetValValGluGlyCy 393
Db 1324 CTTCCAGCACAGCTCTAATGTCTCTCTGAAGAAGTACAGAAACATGGTGGTCCGGGCCTG 1383
Qy 393 sGlyCys 395
Db 1384 TGGCTGC 1390
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Search completed: January 11, 2006, 02:27:57
Job time : 229 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 10, 2006, 23:27:45 ; Search time 3445 Seconds

(without alignments)
5378.138 Million cell updates/sec

Title: US-10-801-648-2

Perfect score: 2098

Sequence: 1 MVAGTRCILLALLPQLVIGG.....NEKVLKNYQDMVVGCGCR 396

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/SUPPIX-rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-DB=EST -QFMT=fastap -SUPPIX-rst -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10801648.CGN 1_1_4015@runat09012006 143119 14778 -NCPU=6 -ICPU=3
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc:*
5: gb_est4:*
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7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2098	100.0	2394	4 CR618407	CR618407 full-length
2	1732	82.6	983	10 AY418812	AY418812 Homo sapi
3	1568	75.7	977	10 AY418814	AY418814 Mus muscu
4	1444	68.8	903	5 BX431362	BX431362 BX431362
5	1339	63.8	841	8 DNI117475	DNI117475 1117145 M
6	1269	60.5	1227	10 AY409113	AY409113 Homo sapi
7	1269	60.5	1676	4 CR595138	CR595138 full-length

8	1269	60.5	1692	4 CNSLTI18E	BX161438 human ful
9	1269	60.5	1705	4 CNSLTI18D	BX161385 human ful
10	1268	60.4	1227	10 AY409115	AY409115 Mus muscu
11	1254.5	59.8	1636	8 CX354839	CX354839 ssalrqb53
12	1234	58.8	724	8 CV804617	CV804617 AGENCOURT
13	1232	58.7	711	10 AY418813	AY418813 Pan trogl
14	1229	58.6	881	5 BU444424	BU444424 603213309
15	1167	55.6	727	5 BU625617	BU625617 UI-H-FGI-
16	1106	52.7	715	7 CK940908	CK940908 4064444 B
17	1077	51.3	1227	10 AY409114	AY409114 Pan trogl
18	1056	50.3	581	3 BP276858	BP276858 BP276858
19	1045	49.8	1001	5 BX432994	BX432994 BX432994
20	1042	49.7	649	3 BQ184625	BQ184625 UI-E-EJ1-
21	1039	49.5	642	3 BM929343	BM929343 UI-E-EJ1-
22	1038	49.5	648	3 BM683313	BM683313 UI-E-EJ1-
23	1035	49.3	711	7 CN396138	CN396138 170004241
24	1029	49.0	666	1 AW332667	AW332667 XZ89F02.X
25	1021	48.7	782	5 BX728232	BX728232 BX728232
26	1015	48.4	761	5 BX728231	BX728231 BX728231
27	1014	48.3	649	3 BQ186599	BQ186599 UI-E-EJ1-
28	1010.5	48.2	830	8 DNI117122	DNI117122 1116761 M
29	1008	48.0	674	3 BM674840	BM674840 UI-E-EJ0-
30	999.5	47.6	867	8 CX315415	CX315415 JGI_XZT55
31	998.5	47.6	780	6 CF286367	CF286367 AGENCOURT
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36	956	45.6	1002	11 CNS041FG	AL292165 Tetraodon
37	948.5	45.2	656	3 B1400982	BI400982 MI-P-Ayl-
38	946	45.1	617	1 AL864240	AL864240 AL864240
39	946	45.1	802	5 BU244511	BU244511 603781223
40	940	44.8	614	9 AZ655571	AZ655571 1M0530C11
41	934	44.5	1115	5 BU114214	BU114214 603130312
42	930.5	44.4	821	7 CR433599	CR433599 CR433599
43	928.5	44.3	898	6 CA454850	CA454850 AGENCOURT
44	921	43.9	533	7 CO610202	CO610202 DGB-90H16
45	917	43.7	526	6 CB132019	CB132019 K-EST0182

RESULT 1

CR618407

LOCUS

DEFINITION full-length cDNA clone CS0DE003YB10 of Placenta of Homo sapiens (human).

ACCESSION CR618407

VERSION CR618407.1 GI:50499214

KEYWORDS HTC; CNSLT cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 2394)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished

CONTACT Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paraday Avenue

2 (bases 1 to 2394)

Genoscope.

Direct Submission

TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

COMMENT

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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Qy	101	ArgAlaAlaSerArgAlaAsnThrValArgSerPheHisHisGluGluSerLeuGluGlu	120
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Qy	121	LeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIlePro	140
Db	720	CTACCAGAACGAGTGGGAAACAAACCCGGAGATTCTCTTTAATTTAAGTTCTATCCCC	779
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Db	780	ACGAGGAGTTTATCACTCTAGCAGAGCTTCAGGTTTTCGAGAACAGATGCAAGATGCT	839
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Db	840	TTAGGAAACAATAGCAGTTTCATCCACCGAATTAATATTTATGAATCATATAACCTGCA	899
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Qy	201	AlaSerArgTTPGluSerPheAspValThrProAlaValMetArgTTPThrAlaGlnGly	220
Db	960	GCAAGCAGTGGGAAAGTTTGTGATGTACCCCGCTGTGATCCGGTGGACTGCACAGGA	1019
Qy	221	HisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSer	240
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Qy	241	LysArgHisValArgIleSerArgSerLeuHisGlnAspGluHisSerTTPSerGlnIle	260
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Qy	261	ArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlu	280
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DEFINITION		genomic survey sequence.	
ACCESSION		AY418812	
VERSION		AY418812.1	GI:39774772
KEYWORDS		GSS.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		1 (bases 1 to 983)	
AUTHORS		Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	
TITLE		Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios	
JOURNAL		Science 302 (5652), 1960-1963 (2003)	
PUBMED		14671302	
REFERENCE		2 (bases 1 to 983)	
AUTHORS		Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	
TITLE		Direct Submission	
JOURNAL		Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
COMMENT		These sequences were made by sequencing genomic exons and ordering them based on alignment.	
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ORIGIN			
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Pred. No.:	1.82e-164	Length:	983
Score:	1732.00	Matches:	326
Percent Similarity:	99.69%	Conservative:	0

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Best Local Similarity: 99.69% Mismatches: 1
Query Match: 82.55% Indels: 0
DB: 10 Gaps: 0

US-10-801-648-2 (1-396) x AY418812 (1-983)

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Db 3 GGGACCCGCTCTCTTCTAGCTTCTCTCCAGGTCCTCTCCGGCGGCGCGCTGCG 62

Qy 24 LeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArgProSerSer 43
Db 63 CTCGTCGCGAGCTGGCGCAGGAGTTCGCGCGGCTGCTCGCGCGCGCTCTCATCC 122

Qy 44 GlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMetPheGlyLeu 63
Db 123 CAGCCCTCTGACGAGTCTCTGACGAGTTCAGTTGCGGCTGCTCAGCATGTTGGCCCTG 182

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Qy 124 ThrSerGlyLysThrArgArgPhePheAenLeuSerSerIleProThrGluGlu 143
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Qy 144 PheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAen 163
Db 423 TTTATCACTCAGCAGAGCTTCAGGTTTTCGAGAAACAGATGCAAGATGCTTTAGGAAAC 482

Qy 164 AenSerSerPheHisArgIleAenIleTyrGluIleIleLysProAlaThrAlaAen 183
Db 483 AATAGCAGTTTCCATCACCGAATTAATATTATGAATCATAAACCTGCACAGCCAAAC 542

Qy 184 SerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArg 203
Db 543 TCGAAATTCCTCCGTCAGCAGCTTTTGGACACAGGTTGGTGAATCAGATGCAAGCAGG 602

Qy 204 TrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAen 223
Db 603 TGGGAAAGTTTTGTATGTACCCCGCTGTGATGCGGTGGAATGCAAGGAGCAGCCAAAC 662

Qy 224 HisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSerLysArgHis 243
Db 663 CATGATTCGTGGTGGAGTGGCCACCTTGGAGGAGAAACAGGTTCTCCAAGAGACAT 722

Qy 244 ValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeu 263
Db 723 GTTAGTAAGCAGAGTCTTTGCACCAAGATGACACAGCTGCTCAGATTAAGCCATTTG 782

Qy 264 LeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGlyLysArgGln 283
Db 783 CTAGTAACTTTTGGCCATGATGGAAGAGGCACTCTCTCCACAAAGAGAGAAACGTCAA 842

Qy 284 AlaLysHisLysGlnArgLysArgLeuLysSerSerSerLysArgHisProLeuTyrVal 303
Db 843 GCCAAACCAACACGCGGAAACGCTTAAGTTCAGCTGTAAAGAGACACCCCTTTGTACGTG 902

Qy 304 AspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisAlaPhe 323
Db 903 GACTTCAGTGAGCTGGGTGGAAATGACTGATTTGGCTTCCCGGGGTATCACGCCCTTT 962

Qy 324 TyrCysHisGlyGluCysPro 330
Db 963 TACTGCCACGAGAAATGCCCT 983
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RESULT 3
AY418814
LOCUS
DEFINITION Mus musculus BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY418814
VERSION AY418814.1 GI:39774774
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 977)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Infering nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED 14671302
REFERENCE
2 (bases 1 to 977)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..977
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>977
/gene="BMP2"
/locus_tag="HMC6682"
gene
ORIGIN
Alignment Scores:
Pred. No.: 6.99e-150 Length: 977
Score: 1588.00 Matches: 295
Percent Similarity: 95.41% Conservative: 17
Best Local Similarity: 90.21% Mismatches: 13
Query Match: 75.69% Indels: 2
DB: 10 Gaps: 2
US-10-801-648-2 (1-396) x AY418814 (1-977)
Qy 4 GlyThrArgCysLeuLeuAlaLeuLeuLeuProGlnValLeuLeuGlyGlyAlaAlaGly 23
Db 3 GGGACCCGCTCTCTTCTAGTGTCTCTCCAGGTCCTCTCCGGCGGCGCGCGCGCG 62
Qy 24 LeuValProGluLeuGlyArgArgLysPheAlaAlaSerSerGlyArgProSerSer 43
Db 63 CTCATTCAGAGCTGGCGCGCAAGATTCGCGCGCATCCAGC---CGACCCCTGTGCC 119
Qy 44 GlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeuSerMetPheGlyLeu 63
Db 120 CGGCTTCGGAAGAGCTCTCAGCAATTTGATTTGAGGCTGCTCAGCATGTTGGCCCTG 179
Qy 64 LysGlnArgProThrProSerArgAspAlaValValProProTyrMetLeuAspLeuTyr 83
Db 180 AAGCAGAGACCCACCCAGCAGCAGCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 239
Qy 84 ArgArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGluArgAlaAla 103
Db 240 CGCAGGCACTCAGGCGCAGCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 299
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Qy 104 SerArgAlaAenThrValArgSerPheHisHisGluGluSerLeuGluLeuProGlu 123
 Db 300 AGCCGCGCCACACCGTGGCGAGCTTCATCAGAGAAAGCGTGGAGAACTTCCAGAG 359
 Qy 124 ThrSerGlyLysThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGlu 143
 Db 360 ATGAGTGGGAAACCGCCGCGCTCTCTTCAATTAAAGTTCTGTCCCGAGTGCAGG 419
 Qy 144 PheIleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsn 163
 Db 420 TTTCTCATCTGCAGAACTCCAGATCTCCGGAACAGATACAGAGAGCTTTGGGA-- 476
 Qy 164 AsnSerSerPheHisHisArgIleAsnIleTyrGluIleLeuLysProAlaThrAlaAsn 183
 Db 477 AACAGTAGTTTCCAGCACCGAATTAATATTATGAATTAAGCTTGCAGAGCCAAAC 536
 Qy 184 SerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArg 203
 Db 537 TTGAATTTCTGTGACAGACTATTGGACACCAAGTTAGTGAATCAGAACACAACTCAG 596
 Qy 204 TrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsn 223
 Db 597 TGGAGAGCTTTCGACGTCACCCAGCTGTGATGCGGTGGACACACAGGGACACACCAAC 656
 Qy 224 HisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSerLysArgHis 243
 Db 657 CATGGGTTTGGTGGAGTGGCCCAATTAGAGAGAACCCAGGTGTCTCCAGAGACAT 716
 Qy 244 ValArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeu 263
 Db 717 GTGAGGATTAGCAGTCTTTGCCACCAAGATGAACACAGCTGTGCACAGATAAGGCCATTG 776
 Qy 264 LeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGluLysArgGln 283
 Db 777 CTAGTGACTTTGGACATCATGAGAAAGGACATCCGCTCCACAAACGAGAAACGCTCAA 836
 Qy 284 AlaLysHisLysGlnArgLysArgLeuLysSerCysLysArgHisProLeuTyrVal 303
 Db 837 GCCAAACACAAACAGCGAAGCGCTCAAGTCCAGCTGCAAGAGACACCCCTTTGTATGTG 896
 Qy 304 AspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisAlaPhe 323
 Db 897 GACTTCAGTGATGGGGTGGATGACTGGATCGTGGACCTCCGGGCTATCATGCCTTT 956
 Qy 324 TyrCysHisGlyLysGluCysPro 330
 Db 957 TACTGCCATGGGAGTGTCTCT 977

RESULT 4
 BX431362
 LOCUS BX431362 903 bp mRNA linear EST 04-MAY-2004
 DEFINITION BX431362 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE003YB10
 5-PRIME, mRNA sequence.
 ACCESSION BX431362
 VERSION BX431362.2 GI:47009531
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 903)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 15, 2003 this sequence version replaced gi:30781021.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 10041.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0BAG0112G10_CS01039_1&c=10041.f.

FEATURES

source

Location/Qualifiers

1..903

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DE003YB10"

/tissue_type="PLACENTA"

/clone_lib="Homo sapiens PLACENTA"

/notes="vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 2,42e-135 Length: 903
 Score: 1444.00 Matches: 280
 Percent Similarity: 96.27% Conservative: 4
 Best Local Similarity: 94.92% Mismatches: 11
 Query Match: 68.83% Indels: 2
 DB: 5 Gaps: 0

US-10-801-648-2 (1-396) x BX431362 (1-903)

Qy 92 SerProAlaProAspHisArgLeuGluArgAlaAlaSerArgAlaAenThrValArgSer 111
 Db 6 GCTCCCGCCGCACACCCCGTTGGGGGGGGGAGCCAGCCGAGCCAC- ACTGTGCGCAGC 64
 Qy 112 PheHisHisGluGluSerLeuGluLeuProGluThrSerGlyLysThrThrArgArg 131
 Db 65 TTCACCATGAGAGAAATCTTTGGAGAACTACCAAGACGAGTGGGAAACAAACCCGGAGA 124
 Qy 132 PhePhePheAsnLeuSerSerIleProThrGluGluPheIleThrSerAlaGluLeuGln 151
 Db 125 TTCTTCTTTAATTAAAGTTCTATCCCGCAGGAGGTTTATCACCTCAGCAGAGCTTTCAG 184
 Qy 152 ValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPheHisHisArgIle 171
 Db 185 GTTTCGAGACACAGATGCAAGATGCTTTAGGAAACAATAGCAGTTTCCATCACCGAATT 244
 Qy 172 AsnIleTyrGluIleIleLysProAlaThrAlaAsnSerLysPheProValThrArgLeu 191
 Db 245 AATATTTATGAAATCATAAACCTGCAACAGCCCACTCGAAATTCCTCCGTGACAGTCTT 304
 Qy 192 LeuAspThrArgLeuValAsnGlnAsnAlaSerArgTrpGluSerPheAspValThrPro 211
 Db 305 TTGGACACCAAGTGTGGTGAATCAGATGCAAGCAGGTGGGAAAGTTTGTATGTCAACCCC 364
 Qy 212 AlavaMetArgTrpThrAlaGlnGlyHisAlaAsnHisGlyPheValGluValAla 231
 Db 365 GCTGTGATGGCGTGGAGTGCACAGGGACACGCCCAACCATGATTCGTTGGTGGAGTGGCC 424
 Qy 232 HisLeuGluGluLysGlnGlyValSerLysArgHisValArgIleSerArgSerLeuHis 251
 Db 425 CACTTGGAGGAGAAACAAGGTGTCTCCAGAGACATGTTAGGATACAGAGTCTTTGGCAC 484
 Qy 252 GlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValThrPheGlyHisAspGly 271
 Db 485 CAAGATCAACACAGCTGTTCACAGATAAGGCCATTGCTAGTAACCTTTTGGCCATGATGGA 544
 Qy 272 LysGlyHisProLeuHisLysArgGluLysArgGlnAlaLysHisLysGlnArgLysArg 291
 Db 545 AAAGGGCATCTCTCCCAAAAAAGAGAAAAACGTCAGCCCAACCAACCAACCGGAAACGC 604
 Qy 292 LeuLysSerSerCysLysArgHisProLeuTyrValAspPheSerAspValGlyTyrAsn 311

Db 605 CTTAAGTCCAGCTGTAAAGACACACCCCTTTGTACGTGGAGCTTCAGTGCAGTGGGGTGAAT 664
 QY 312 AsptTolileValAlaProGlyTyrHisAlaPheTyrCysHisGlyGluCysProPhe 331
 Db 665 GACTGGATTGGGCTCCCGGGGTATCACGCTTTTACTGCCAGAGAATGCCCTTTT 724
 QY 332 ProLeuAlaAspHisLeuAsnSerThrAsnHisAlaIleValGlnThrLeuValAsnSer 351
 Db 725 CCTCGGCTGATCATCTCACTCCACTAATCATGCCATTGTCAGACGTTGGTCACTCT 784
 QY 352 ValAsnSerLysIleProLysAlaCysCysValProThrGluLeuSerAlaIleSerMet 371
 Db 785 GTTAACTCTAAGATTCCTAAGCACTGTGTGCCGACAGAACTCAGTGTCTATCTCGATG 844
 QY 372 LeuTyrLeuAspGluAsnGluLysValValLeuLysAsnTyrGln 386
 Db 845 CTGTACCTTTGACGAGATGA-AAGGTTGTATTAAAGAACTTCAGA 888

RESULT 5
 DN117475/c 841 bp mRNA linear EST 15-FEB-2005
 LOCUS DN117475
 DEFINITION 1117145 MARC 4PIG Sus scrofa CDNA 3', mRNA sequence.
 ACCESSION DN117475
 VERSION DN117475.1 GI:59811735
 KEYWORDS EST.

SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.

REFERENCE 1 (bases 1 to 841)
 AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
 Nonneman,D.J., Wray,J.E. and Keele,J.W.
 TITLE Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages

JOURNAL Unpublished (2003)
 COMMENT Contact: Smith TPL
 USDA, ARS US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.

Plate: HHY8017 row: A column: 20
 Seq primer: TAGAAGGCACAGTCGAGG.

FEATURES

Location/Qualifiers
 1..841
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH108"
 /clone_lib="MARC 4PIG"
 /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
 Library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

ORIGIN

Alignment Scores:
 Pred. No.: 9,45e-125 Length: 841
 Score: 1339.00 Matches: 248
 Percent Similarity: 95.83% Conservative: 5
 Best Local Similarity: 93.94% Mismatches: 11
 Query Match: 63.82% Indels: 0
 DB: 8 Gaps: 0

US-10-801-648-2 (1-396) x DN117475 (1-841)

QY 133 PhePheAsnLeuSerSerIleProThrGluGluPheIleThrSerAlaGluLeuGlnVal 152
 Db 839 TTTTAAATTAACTCTCTGTCCTCCCGAGGAGTTATTCATTCAGCAGAACTTCAGGTC 780

QY 153 PheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPheHisHisArgIleAsn 172
 Db 779 TTTTCGGACACAGACACAGGAGACTTTGGATAACAGTAGACAGTTTCCATCACCAGATTAAAT 720
 QY 173 IleTyrGluIleIleLysProAlaThrAlaAsnSerLysPheProValThrArgLeuLeu 192
 Db 719 ATNTATGAATCATCAAACTGCAACAGCCAACTCCAGATTCCCGGTGACAGACTTTTG 660
 QY 193 AspThrArgLeuValAsnGlnAsnAlaSerArgTTPGluSerPheAspValThrProAla 212
 Db 659 GACACCAAGTTGGTGACTCCGAATGCCAGAGGTGGAGAGCTTCGAGCTACCCCGCT 600
 QY 213 ValMetArgTTPThrAlaGlnGlyHisAlaAsnHisGlyPheValValGluValAlaHis 232
 Db 599 GTGATGCGGTGGACTGCACACGGGGTGCACACGGGGTTCGTGGTGGAGTGGCCAC 540
 QY 233 LeuGluLysGlnGlyValSerLysArgHisValArgIleSerArgSerLeuHisGln 252
 Db 539 CCGGAGGACACGCCCGAGGTCTCCAAGAGGATGTGCGGATTAGCAGGTCTTTGCACCA 480
 QY 253 AspGluHisSerTTPSerGlnIleArgProLeuLeuValThrPheGlyHisAspGlyLys 272
 Db 479 GATGAGCACAGCTGGTCAAAATAGACCTTGTCTAGTCACTTTCCGCCACGATGGGAA 420
 QY 273 GlyHisProLeuHisLysArgGluLysArgGlnAlaLysHisLysGlnArgLysArgLeu 292
 Db 419 GGACACCTCTGCACAAAGGGAAGGTCACGACAAACACACAGCGCAAGCGCTG 360
 QY 293 LysSerSerCysLysArgHisProLeuTyrValAspPheSerAspValGlyTTPAsnAsp 312
 Db 359 AAATCCAGCTGCAAGAGACACCTTTGTACGTGGACTTCAGTGTGGCTGGGAATGAC 300
 QY 313 TrpIleValAlaProGlyTyrHisAlaPheTyrCysHisGlyGluCysProPhePro 332
 Db 299 TGGATCGTAGCCCCCGGGGTATCATGCCCTTTTACTCCACGGGAGTGCCCTTTCCCC 240
 QY 333 LeuAlaAspHisLeuAsnSerThrAsnHisAlaIleValGlnThrLeuValAsnSerVal 352
 Db 239 CTGGCTGATCACTGNACTCCACGNAATCAGCCCATCGTCCAGACCTTGGTCAACTCGTT 180
 QY 353 AsnSerLysIleProLysAlaCysCysValProThrGluLeuSerAlaIleSerMetLeu 372
 Db 179 AACTCTAAGATCCCAAGCGGTGCTGTGTCTCCACAGAACTCAGTGCCTCATCTGCTG 120
 QY 373 TyrIleAspGluAsnGluLysValValLeuLysAsnTyrGlnAspMetValValGluGly 392
 Db 119 TACCTTGACGAGAACGAAAGGTGTATTAAAGAACTACAGGACATGTTGTGGAGGT 60
 QY 393 CysGlyCysArg 396
 Db 59 TGTGGGTGTCTGT 48

RESULT 6
 AY409113 1227 bp DNA linear GSS 16-DEC-2003
 LOCUS AY409113
 DEFINITION Homo sapiens BMP4 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION AY409113
 VERSION AY409113.1 GI:39765081
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 1227)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Gargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios


```

division of Invitrogen.
FEATURES             Location/Qualifiers
     source           1..1676
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CSODI042YJ24"
                     /tissue_type="Placenta"
                     /plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.:          3,22e-117      Length:          1676
Score:              1269.00         Matches:         258
Percent Similarity: 73.19%         Conservative:    45
Best Local Similarity: 62.32%       Mismatches:     87
Query Match:        60.49%         Indels:         24
DB:                  4              Gaps:          10

US-10-801-648-2 (1-396) x CR595138 (1-1676)

Qy      1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyCly 20
Db      184 ATGATTCCTGTAACCGAATGCTGATGTCGTCTTTATTATCCAAAGTCCTCTAGGAGGC 243
Qy      21 Ala-----AlaGlyLeuValProGluLeuGlyArgArgGlyPheAla-----Ala 35
Db      244 CGAGCCATGCTAGTTGATACCTGAGACGGGGAGAAAAGTCGCCGAGATTCAGGGC 303
Qy      36 AlaSerSerGlyArgProSerSerGlnProSerAspGluValLeuSerGluPheGluLeu 55
Db      304 CACGCGGGAGGAGCGCGCTCAGGGCAG---AGCCATGAGCTCCTCGGGGACTTCGAGGCG 360
Qy      56 ArgLeuLeuSerMetPheGlyLeuLeuGlnArgProThrProSerArgAspAlaValVal 75
Db      361 ACACCTTCCTGCAGATGTTTGGGCTGGCGCGCGCGCGAGCTAGCAAGAGTGCCTGATT 420
Qy      76 ProProTyrMetLeuAspLeuTyrArgArgHisSerGlyGln----- 89
Db      421 CCGGACTACATGCGGGATCTTTACCGGCTTCAGTCTGGGGAGGAGGAGGAGAGCAGATC 480
Qy      90 -----ProGlySerProAlaProAspHisArgLeuGluArgAlaAlaSerArgAlaAsn 107
Db      481 CACAGCAGCTGCTTGAGTATCCT-----GAGCGCGCGCGCGCGAGCGGCGCAAC 528
Qy      108 ThrValArgSerPheHisGlyGluSerLeuGluLeuProGluThrSerGlyLys 127
Db      529 ACCGTGAGGAGCTTCACCCAGAGAACATCTGGAGAACATCCCGAGGACCAAGTGAAC 588
Qy      128 ThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGluPheIleThrSer 147
Db      599 TCTGCTTTTCTTCTCTTTAACTCAGACAGCATCCTCTGAGACAGAGTGAATCTCTCT 648
Qy      148 AlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerSerPhe 167
Db      649 GCAGAGCTTCGGCTCTTCGGGAGCAGGTGGACACAGGGCCCTGATTGGGAAAGGGGCTTC 708
Qy      168 HisHisArgIleAsnIleTyrGluIleIleLys-----ProAlaThrAlaAsnSerLysPhe 186
Db      709 ---CACCGTATAAACATTATGAGGTATTGAGGCCCGCCAGCAGAGAGTGGTCCCTGGGCAC 765
Qy      187 ProValThrArgLeuLeuAspThrArgLeuValLeuGlnAsnAlaSerArgTyrGluSer 206
Db      766 CTCATCACAGCACTACTGACACAGACTGGTCCACCAATGTGCACACGGTGGGAAACT 825
Qy      207 PheAspValThrProAlaValMetArgTyrThrAlaGlnGlyHisAlaAsnHisGlyPhe 226
Db      826 TTTGATGTGAGCCCTCGGGTCTCTCGCTGGACCGCGGAGAGACACCCAACTATGGGCTA 885
Qy      227 ValValGluValAlaHisLeuGluGlyGlnGlyValSerLysArgHisValArgIle 246
Db      886 GCCATTGAGGTGACTCAGCTCCATCAGACTCGGACCCACCGAGCGGCGCAGCATGTCAAGATT 945

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247 SerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuLeuValThr 266

946 AGCCGATCGTTACCTCAAGGGAGTGGGAATTTGGCCAGCTCCGCCCTCTCTGGTCAAC 1005

267 PheGlyHisAspGlyLysGlyHisProLeu-----HisLysArgGluLysArgGlnAla 284

1006 TTTGGCCATGATGCCCGGGGCCATGCTTGACCCGACGCGCGAGGGGCCAAGCGTAGCCCT 1065

285 Lys---HisLysGlnArgLysArgLeuLysSer---SerCysLysArgHisGlyProLeuTyr 302

1066 AAGCATCACTCACAGCGGGCCAGGAGAGAGATTAAGAACTGCCGGGCCCATCTCGTCTAT 1125

303 ValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGlyTyrHisAla 322

1126 GTGGACTTCAGCGATGTGGCTGCAATGATGATTTGGGCCCAACACAGGCTACCCAGGCC 1185

323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis 342

1186 TTCTACTGCCATGGGAGTGCCTTTCCACTGCTGACCACTCAACTCAACCAACCAT 1245

343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362

1246 GCCATTGTGCAGACCTTGGTCATCTGTCATTCAGTATCCCAAGACCTGTGTGTG 1305

363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValValLeu 382

1306 CCCACTGAAGTGAAGTGCATCTCCATGCTGATCTGATGATGATGATGATGATGATGATG 1365

383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396

1366 AAAAAATTATCAGGAGATGGTAGTAGAGGATGTGGTGGCCGC 1407

RESULT 8

CNSLT118E 1692 bp mRNA linear HTC 28-JAN-2003

LOCUS human full-length cDNA clone CSODI018YL16 of Placenta of Homo

DEFINITION sapiens (human).

ACCESSION BX161438

VERSION BX161438.1 GI:28071055

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1692)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Paraday Avenue PO Box 6482 Carlsbad, California, 92008 Phone : +1 760 603-7200

REFERENCE 2 (bases 1 to 1692)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT - Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

Location/Qualifiers

1..1692

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI018YL16"

/tissue_type="Placenta"

/plasmid="pCMVSPORT_6"

/note="Cot 25-normalized"


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/clone="CSODC002YH22"
/tissue_type="Neuroblastoma"
/plasmid="pCMVSPORT.6"
/notes="Cot 25-normalized"
188..1414
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/codon_start=1
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RRSGSHLLDFRATLQMFGLRRRPPQSAVIPDMRLYLRLQSEEEBEEQIHS
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FREVDQDQWERGFHRLINIYVWKPFAEYVPGHLITRLDLRLVHNHVRWTFDVS
PAVLRTKQPNYGLALEVTHLQTRTHQCHVRISRLPQSGSNWAOLRPLLVTFG
HDSGHALTTRRARRKSPKHSQARKKNCRSHLYVDFSDVGNWDMIVAPGYQA
FYCHGDCFPFLADHLNSTHALVQTLVNSVNSPIPKACCVTELSAISMLYDHYDKV
VLKNYQEMVVEGCGR"

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ORIGIN

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Alignment Scores:
Pred. No.: 3,3e-117 Length: 1705
Score: 1269.00 Matches: 258
Percent Similarity: 73.19% Conservative: 45
Best Local Similarity: 62.32% Mismatches: 87
Query Match: 60.49% Indels: 24
DB: 4 Gaps: 10

US-10-801-648-2 (1-396) x CNSLTI18D (1-1705)
QY 1 MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly 20
Db 188 ATGATTCCTGGTAACCGAATGCTGATGGTGGTCTTTATTATGCAAGTCTCTGTCAGAGGC 247
QY 21 Ala-----AlaGlyLeuValProGluLeuGlyArgArgLysPheAla-----Ala 35
Db 248 GCGAGCCATGCTAGTTGATACCTCAGACGGGGAAGAAAAAGTCGCGGAGATTTCAGGCG 307
QY 36 AlaSerSerGlyArgProSerSerGlnProSerAspGluValLeuSerGluPheGluLeu 55
Db 308 CACGCGGAGGACCGCGCTCAGGCGG---AGCCATGAGCTCTCTCGGCGACTTCGAGCGG 364
QY 56 ArgLeuLeuSerMetPheGlyLeuLysGlnArgProThrProSerArgAspAlaValVal 75
Db 365 ACACCTTCGCAGATGTTGGGTGGCGCGCGCGCGAGCTTACGACAGAGTGCCTGATC 424
QY 76 ProProTyrMetLeuAspLeuTyrArgArgHisSerGlyGln----- 89
Db 425 CCGGACTACATCGCGGATCTTTACCGGCTTCAGTCTGGGGAGGAGGAGGAGCAGATC 484
QY 90 -----ProGlySerProAlaProAspHisArgLeuGluArgAlaAlaSerArgAla 107
Db 485 CACAGCAGCTGGTCTTGAGTATCT-----GAGCGCGCGCGCGAGCGCGGCGCAAC 532
QY 108 ThrValArgSerPheHisGlyGluSerLeuGluLeuProGluThrSerGlyLys 127
Db 533 ACCGTGAGAGAGCTTCACCCAGAGACATCTGGAGACATCCCGAGGACCATGAAAC 592
QY 128 ThrThrArgArgPhePhePheAsnLeuSerSerIleProThrGluPheIleThrSer 147
Db 593 TCTGCTTTTCTCTCTTTAACTCAGCAGCATCCCTTGAGAACGAGGTGATCTCTCT 652
QY 148 AlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsnSerPhe 167
Db 653 GCAGAGCTTCGCTCTTCGCGAGCAGGTGGACCGGCGCTGATGGGAAAGGGGCTTC 712
QY 168 HisHisArgIleAsnIleTyrGluIleIleLys---ProAlaThrAlaAsnSerLysPhe 186
Db 713 ---CACCGTATTAACATTATGAGGTATGAGGCCCGCAGAGAGTGTGCTGGGCAC 769
QY 187 ProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTrpGluSer 206
Db 770 CTCATCACAGGACTACTGCAGCAGGAGACTGGTCCACCAATGTGACACGGTGGGAAACT 829

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QY 207 PheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsnHisGlyPhe 226
Db 830 TTTGATGTGAGCCTCGCGTCTTTGCTGGACCGGAGAGACGACCAAACTATGGGCTA 889
QY 227 ValValGluValAlaHisLeuGluGlyGlnGlyValSerLysArgHisValArgIle 246
Db 890 GCCATTGAGGTGACTACCTCATCAGCTCGGACCCACCGGCGGCGACGATGTGAGGATT 949
QY 247 SerArgSerLeuHisLeuAspGluHisSerTrpSerGlnIleArgProLeuLeuValThr 266
Db 950 AGCCGATCGTTACTCAAGGAGTGGGATTTGGGCCCGAGCTCCGCGCCCTCTCTGGTCACC 1009
QY 267 PheGlyHisAspGlyLysGlyHisProLeu-----HisLysArgGluLysArgGlnAla 284
Db 1010 TTTGGCCATGATGCGCGGGCCATGCTTACCGACGCGCGGAGGGCCGCAAGCGTAGCCCT 1069
QY 285 Lys---HisLysGlnArgLysArgLeuLysSer---SerCysLysArgHisProLeuTyr 302
Db 1070 AAGCATCACTCACAGCGCGGCCAGGAAGAATAAGAACTCCGCGGCCCACTCGCTCTAT 1129
QY 303 ValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProGlyTyrHisAla 322
Db 1130 GTGGACTTCACGATGCGGCTGGATGACTGGATTTGGGCCCGCCACGAGGTACCGAGGCC 1189
QY 323 PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis 342
Db 1190 TTCTACTGCCATGGGACTGCCCTTTCCACTGGCTGACCACTCAACTCAACCAACCAT 1249
QY 343 AlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAlaCysCysVal 362
Db 1250 GCCATTGTGCAGACCCCTGGTCAATTCTGTCAATTCAGATATCCCAAGCCCTGTTGTGTG 1309
QY 363 ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValValLeu 382
Db 1310 CCCACTGAACGTAGTGCCATCTCCATGCTGACCTGGATGATGATGATGATGATGATGATG 1369
QY 383 LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
Db 1370 AAAAATTATCAGGAGATGTTAGAGGATGTTGGTGCGCGC 1411

RESULT 10
AY409115 1227 bp DNA linear GSS 16-DEC-2003
LOCUS Mus musculus BMP4 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY409115
VERSION AY409115.1 GI:39765083
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Mus;
REFERENCE 1 (bases 1 to 1227)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1227)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers

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/note=Vector: pQWspore6; Library Creator: Research Genetics ; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Uh, and Robert Devlin (DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seapring Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)"

ORIGIN

Alignment Scores:
 Pred. No.: 9,15e-116 Length: 1636
 Score: 1254.50 Matches: 252
 Percent Similarity: 73.19% Conservative: 51
 Best Local Similarity: 60.87% Mismatches: 86
 Query Match: 59.80% Indels: 25
 DB: 8 Gaps: 11

US-10-801-648-2 (1-396) x CX354839 (1-1636)

Qy	1	MetValAlaGlyThrArgCysLeuLeuAlaLeuLeuProGlnValLeuLeuGlyGly	20
Db	398	ATGATTCCTGGTAATCGAATCGATGTCATTTTATTATGCCAAGTCCTGCTGGGAGAG	457
Qy	21	Ala-----AlaGlyLeuValProGluLeuGlyArgArgGlyPheAlaAlaSerSer	38
Db	458	AGCAACCATGCTAGTCTGATACCTGAGGAAGGGAAGAGAA--GCACCGGGGCTGCAG	514
Qy	39	GlyArgProSerSerGlnProSerAspGluValLeuSerGluPheGluLeuArgLeuLeu	58
Db	515	AGCCGGACTGCTGGTCAG--AGCATGACTGCTCGGGACTTTTGAGCCACGCTGCTA	571
Qy	59	SerMetPheGlyLeuLeuGlnArgProThrProSerArgAspAlaValValProProTyr	78
Db	572	CACATGTTGGACTGCAGAGCGCGCGCCAGTCGCTCGGCACCTGTGCCACGGTAC	631
Qy	79	MetLeuAspLeuTyrArgArgHisSerGlyGlnProGlySerProAlaProAspHisArg	98
Db	632	CTGCTGGACCTCTACCGCTCGAGTCGGCGCGAG--GCTGAGGAGCGCGCCACCCACGAC	688
Qy	99	Leu-----GluArgAlaAlaSerArgAlaAenThrValArgSerPheHis	113
Db	689	ACCGCTTTGAGTACCCGAGGTCGGCTAGCGCGCAACACCGTGGGGGCTTCCAC	748
Qy	114	HisGluGluSerLeuGluGluLeuProGluThrSerGlyLysThrArg-----	130
Db	749	CACGAGACACATGAGCCGGTTCATCCGGCGAGTCTCAGACGAAGACGAGAGGCC	808
Qy	131	-----ArgPhePheAsnLeuSerSerIleProThrGluGluPheIleThrSer	147
Db	809	ATCCCACTGCGCTTCTCTCAATCTCAGCAACATCCACGAGGAGCGAGCTGCTCTGTCG	868
Qy	148	AlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeu-----GlyAsn	163
Db	869	GCCGAGCTGCGTCTCTCCGAGCAGATCGACGAGGCCATTCGGAAGCGAGGGGAC	928
Qy	164	AsnSerSerPheHisArgIleAsnIleTyrGluIleIleLysProAlaThrAlaAsn	183
Db	929	AAGGATCAGCTC--CACCGATAACCTGTACGAGGTGCTGACGCCCGCGGGCGGG	985
Qy	184	SerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArg	203
Db	986	CAGCTA-----ATCACCGCGCTTTTGGACACACGCTGTCACCATACGCTCGCGC	1039
Qy	204	TrpGluSerPheAspValThrProAlaValMetArgTyrThrAlaGlnGlyHisAlaAsn	223
Db	1040	TGGGAGAGCTTTGAGCTGAGCCCCCGCTGTCGCTGACACCGGGCGCTGCCCCAAC	1099
Qy	224	HisGlyPheValValAlaHisLeuGluGluLysGlnGlyValSerLysArgHis	243
Db	1100	TACGGGCTGGCGCTGAGGTCCAGCCTCAACACGACACCCAGCCACCGGGCGGCCAC	1159
Qy	244	ValArgIleSerArgSerLeuHisGlnAspGlu---HisSerTrpSerGlnIleArgPro	262
Db	1160	CTGCGCATCAGCGCTCGCTGCGACGAGGCGCGGGGAGGACTGGGAGCAGCTAGCGCCC	1219

Qy	263	LeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGluLysArg	282
Db	1220	CTGCTGCTACCTTCGGCCCATGACGCGCAAGGGCCACCGTTGACGCGTGGACCAAGCGC	1279
Qy	283	GlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisProLeuTyr	302
Db	1280	AGCCAAAGCAGCGGGGGCGTAAGCGC---AACCGCAACTGTGCGCGTCATGCTCTCTAC	1336
Qy	303	ValAspPheSerAspValGlyTyrAsnAspTyrIleValAlaProProGlyTyrHisAla	322
Db	1337	GTGGACTTCAGCATGTAGCTGGATGACTGGATAGTGGCGCCGCCAGGTCACGAGCA	1396
Qy	323	PheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSerThrAsnHis	342
Db	1397	TACTACTGCCATGGGAATGTCCCTTCCCTGCGCAGACCACTTACCAACCCAC	1456
Qy	343	AlaIleValGlnThrIleuValAsnSerValAsnSerLysIleProLysAlaCysCysVal	362
Db	1457	GCCATTGTTGAGAGCTTTGGTGAATCTCGGTGAACCAACCATTTCCCAAGGCTGCTGCGTG	1516
Qy	363	ProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLysValValLeu	382
Db	1517	CCACGAGGCTCAGTGCATCTCCATGCTTACTTGGACGACACGACAGTGGTCTCTA	1576
Qy	383	LysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg	396
Db	1577	AAAACTACCAGGAATGTTGTGAAGGGTGTGGCTGCCGC	1618

RESULT 12

CV804617 724 bp mRNA linear EST 15-NOV-2004
 LOCUS AGENCOURT 36361580 NIH MGC 280 Homo sapiens cDNA clone
 DEFINITION IMAGE_7503800 5', mRNA sequence.

ACCSSION CV804617.1 GI:55747583

VERSION EST.

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 724)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Meri Firpo

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLM15873 row: h column: 06

High quality sequence stop: 598.

FEATURES

Location/Qualifiers

1..724

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:7503800"

/tissue type="pluripotent cell line derived from

blastocyst inner cell mass"

/lab host="DH10B"

/clone_lib="NIH MGC 280"

/note="Organ: Blastocyst; Vector: pExpress-1; Site_1:

EcoRV; Site 2: NotI; RNA obtained from pluripotent cell

line derived from blastocyst inner cell mass (cell line

HSP-6, NIH Registry designation UC06. Positive for OCT4

expression by rtPCR, positive for SSEA-3, SSEA-4, TRA-1-81, TRA-1-60 by immunofluorescence. Negative for SSEA-1 by immunofluorescence passage 62. cDNA was primed using oligo-dT primer:
5'-pGACTAGTCTAGACGAGCGCGCCGCTC(T)25-3' and cloned into the EcorV/NotI sites of pExpress-1. Size-selection >1.25 kb resulted in an average insert size of 1.8 kb. This primary library is non-normalized (normalized primary library is NIH MGC 281) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene Collection library."

ORIGIN

Alignment Scores:
Pred. No.: 3,29e-114 Length: 724
Score: 1234.00 Matches: 236
Percent Similarity: 97.93% Conservative: 0
Best Local Similarity: 97.93% Mismatches: 5
Query Match: 58.82% Indels: 1
DB: 8 Gaps: 0

US-10-801-648-2 (1-396) x CV804617 (1-724)

Qy 85 ArgHisSerGlyGlnProGlySerProAlaProAspHisArgLeuGluArgAlaAlaSer 104
Db 1 AGGCACCTCGGTCAGCGGGCTCACCCGCCACAGCCCGTTGGAGAGCGCAGCCAGC 60

Qy 105 ArgAlaSerThrValArgSerPheHisHisGluGluSerLeuGluLeuProGluThr 124
Db 61 CGAGCCCAACACTGTCGCGAGCTTCACCATGAAGAACTTTGGAGAACTACCAAGAACG 120

Qy 125 SerGlyLysThrThrArgArgPhePheAsnLeuSerSerIleProThrGluGluPhe 144
Db 121 AGTGGAAACACCCCGAGATCTCTTAAATTAAGTCTATCCCCACGAGAGGTTT 180

Qy 145 IleThrSerAlaGluLeuGlnValPheArgGluGlnMetGlnAspAlaLeuGlyAsnAsn 164
Db 181 ATCACTCAGCAGAGCTTCAGTTTTCGAGAACAGATGCAAGATGCTTAGGAAACAAT 240

Qy 165 SerSerPheHisHisArgIleAsnIleTyrgluilelelyserProAlaThrAlaAsnSer 184
Db 241 AGCAGTTTCCATCACCCGAATTAATTTATGAATATATAAACTGCAACAGCCAACTCG 300

Qy 185 LysPheProValThrArgLeuLeuAspThrArgLeuValAsnGlnAsnAlaSerArgTrp 204
Db 301 AAATCCCGTGACAGCTCTTTGGACCCAGGTGGTGGATCAGATGCAAGCAGGTGG 360

Qy 205 GluSerPheAspValThrProAlaValMetArgTrpThrAlaGlnGlyHisAlaAsnHis 224
Db 361 GAAAGTTTGTATGTCAACCCCGCTGTGTGCGGTGGACTGCACAGGACAGCCCAACCAT 420

Qy 225 GlyPheValValGluValAlaHisLeuGluGluLysGlnGlyValSerLysArgHisVal 244
Db 421 GGATTCTGTGTGAAGTGGCCCACTTGGAGAGAAACAAGGTGTCTCCAAGACATGTT 480

Qy 245 ArgIleSerArgSerLeuHisGlnAspGluHisSerTrpSerGlnIleArgProLeuLeu 264
Db 481 AGGATAGCAGGCTCTTGGACCAAGATGAACACAGCTGGTGCACAGATAAGGCCAATTGCTA 540

Qy 265 ValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArgGluLysArgGlnAla 284
Db 541 GTAACCTTTGGCCATGATGGAAGGGCATCTCTCCACAAAGAGAAACGTCAGACC 600

Qy 285 LysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHisProLeuTyValAsp 304
Db 601 AAACACAAACAGCGGAAACGCTTAAAGTCCAGCTGTGAAGACACACCCCTTTGACGTGGAC 660

Qy 305 PheSerAspValGlyTTrpAsnAspTrpIleValAlaProProGlyTyHisAlaPheTy 324
Db 661 TTCAGTGGAGTGGGTGGAATGACGGGATTTGTGCTCCCTCCCGGGGAT-CACGCCCTTTTAC 719

325 Cys 325

720 TGC 722

RESULT 13
AY418813
LOCUS
DEFINITION
Pan troglodytes BMP2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY418813
ACCESSION
VERSION
AY418813.1 GI:39774773
SOURCE
GSS.
ORGANISM
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pan.
REFERENCE
1 (bases 1 to 711)
AUTHORS
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 711)
AUTHORS
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
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1..711
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene
<1..>711
/gene="BMP2"
/locus_tag="HCM682"
ORIGIN
Alignment Scores:
Pred. No.: 5,11e-114 Length: 711
Score: 1232.00 Matches: 230
Percent Similarity: 97.88% Conservative: 1
Best Local Similarity: 97.46% Mismatches: 5
Query Match: 58.72% Indels: 0
DB: 10 Gaps: 0

US-10-801-648-2 (1-396) x AY418813 (1-711)

Qy 117 SerLeuGluGluLeuProGluThrSerGlyLysThrThrArgArgPhePheAsnLeu 136
Db 3 TCCTTGGAGAGCTTACCGAAACGAGTGGGAAACACCCGGAGATCTCTTCAATTTA 62

Qy 137 SerSerIleProThrGluGluPheIleThrSerAlaGluLeuGlnValPheArgGluGln 156
Db 63 AGTTCTATCCCCCGAGGAGTCTATCACTCAGCAGAGCTTCAGGTTTTTCGAGAACAG 122

Qy 157 MetGlnAspAlaLeuGlyAsnAsnSerSerPheHisHisArgIleAsnIleTyrgluile 176
Db 123 ATGCGAGATGCTTTAGGAAACAATAGCAGTTTCATCCACCGAAATTAATTTATGAATC 182

Qy 177 IleLysProAlaThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeu 196
Db 183 ATAAACCTCAACAGCCAACTCGAAATTCCTCGTACACAGACTTTTGGACACAGGTTG 242

Qy 197 ValAsnGlnAsnAlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrp 216
Db 243 GTGAATCAGAATGCAAGCAGGTGGGAAAGTTTTTGATGTCAACCCCGCTGTGATCGGTGG 302


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Db      785 AGAACTATCAGATATGTTGTGGAGGCTCGGGTGGCGT 826
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RESULT 15
BU625617/c
LOCUS
DEFINITION
  BU625617
  UI-H-FG1-bgn-b-18-0-UI-s1 NCI CGAP_FG1 Homo sapiens cDNA clone
  UI-H-FG1-bgn-b-18-0-UI 3', mRNA sequence.
ACCESSION
  BU625617
VERSION
  BU625617.1 GI:23291832
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
  1 (bases 1 to 727)
REFERENCE
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
JOURNAL
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps-r@mail.nih.gov
COMMENT
  Tissue Procurement: James Martin
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Clone distribution information can be obtained
  from Dr. M. Bento Soares, bento-soares@uiowa.edu
  The following repetitive elements were found in this cDNA
  sequence: 1-27, >POLY A#Simple_repeat (matched complement) 31-61,
  >(TA)#Simple_repeat (matched complement)
  Seg primer: M13 FORWARD
  POLYA=Yes.
FEATURES
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    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clones="UI-H-FG1-bgn-b-18-0-UI"
    /tissue_type="Cell lines"
    /dev_stage="Adult"
    /lab_host="DH10B (Life Technologies)"
    /clone_lib="NCI-CGAP_FG1"
    /note="Organ: Enchondroma; Vector: p7T3-Pac (Pharmacia)
    with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
    NCI CGAP_FG1 is a normalized cDNA library obtained from a
    pool of mRNA from 2 cell lines from Enchondroma tissues.
    The library was constructed according to Bonaldo, Lennon
    and Soares, Genome Research, 6:791-806, 1996. First strand
    cDNA synthesis was primed with an oligo-dT primer
    containing a Not I site. Double stranded cDNA was ligated
    to an EcoR I adaptor, digested with Not I, and cloned
    directionally into p7T3-Pac vector. The oligonucleotide
    used to prime the synthesis of first-strand cDNA contains
    a library tag sequence that is located between the Not I
    site and the (dT)18 tail. The sequence tag for this
    library is CGGTCACTC. The cell lines were provided by Dr.
    James Martin from the University of Iowa.
    TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
    TAG_L18=UI-H-FG1
    TAG_SEQ=CGGTCACTC"
  ORIGIN
    Alignment Scores:
      Pred. No.: 2,03e-107 Length: 727
      Score: 1167.00 Matches: 214
      Percent Similarity: 99.08% Conservative: 1
      Best Local Similarity: 98.62% Mismatches: 2
      Query Match: 55.62% Indels: 0
      DB: 5 Gaps: 0
  US-10-801-648-2 (1-396) x BU625617 (1-727)

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Search completed: January 11, 2006, 02:09:20

Job time : 3462 secs

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Qy      180 AlaThrAlaAsnSerLysPheProValThrArgLeuLeuAspThrArgLeuValAsnGln 199
      726 GCAACAGCCAACTCGAAATTCNCGTGCACCACTTTGTGGCACCACAGGTTGGTGAATCAG 667
      200 AsnAlaSerArgTrpGluSerPheAspValThrProAlaValMetArgTrpThrAlaGln 219
      666 AATGCAAGCAGGTGGGAAAGTTTGTATGTACCCCTGTGTATGCGGTGACTTGCACAG 607
      220 GlyHisAlaAsnHisGlyPheValValGluValAlaHisLeuGluGluLysGlnGlyVal 239
      606 GGCACGCCCAACCATGGATTCTGTGTGAAGTGGCCCACTTGGAGGAGAAACAAGGTGTC 547
      240 SerLysArgHisValArgLleSerArgSerLeuHisGlnAspGluHisSerTrpSerGln 259
      546 TCCAAAGACATGTTAGGATAAGCAGGCTCTTGCACCAAGATGAACACACAGCTGTGTACAG 487
      260 IleArgProLeuLeuValThrPheGlyHisAspGlyLysGlyHisProLeuHisLysArg 279
      486 ATTAGGCCATGTAGTAACTTTTGGCCATGTATGAAAAGGGCATCTCTCCACAAAGA 427
      280 GluLysArgGlnAlaLysHisLysGlnArgLysArgLeuLysSerSerCysLysArgHis 299
      426 GAAAAACGTCAAGCCAAACACAAACAGCGGAAACGCCTTAAGTCCAGCTGTAGAGACAC 367
      300 ProLeuTyrValAspPheSerAspValGlyTrpAsnAspTrpIleValAlaProProGly 319
      366 CTTTGTACGTGGACTTTCAGTGCAGTGGGTGGAATGACTGGATTTGGTCTCCCGGGG 307
      320 TyrHisAlaPheTyrCysHisGlyGluCysProPheProLeuAlaAspHisLeuAsnSer 339
      306 TATCAGCCCTTTTACTCCACGAGGAATGCCCTTTCTCTGGCTGATCATCTGAACTCC 247
      340 ThrAsnHisAlaIleValGlnThrLeuValAsnSerValAsnSerLysIleProLysAla 359
      246 ACTAATCATGCCATTGTTTCAGACGTTGGTCACTCTGTAACTCTAAGATTCTTAAGSCA 187
      360 CysCysValProThrGluLeuSerAlaIleSerMetLeuTyrLeuAspGluAsnGluLys 379
      186 TGCTGTGTCCCGACAGAACTCAGTGTATCTCGATGCTGTACCTTGACGAGAAATGAAAAG 127
      380 ValValLeuLysAsnTyrGlnAspMetValValGluGlyCysGlyCysArg 396
      126 GTTGTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTGCG 76

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